

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases: older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).  
Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2005, 00:09:54 ; Search time 10 Seconds  
(without alignments)  
104.265 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAFVFLNAPKNTWYAGG.....DRRVEIEVKGKVVTPQAG 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
1: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
2: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
7: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	5.2	417	1	US-10-858-730-227
2	93.5	5.1	229	1	US-10-510-386-228
3	93	5.1	410	1	US-10-793-626-3258
4	93	5.1	477	1	US-10-793-626-3250
5	84	4.6	1992	7	US-11-013-759-3
6	84	4.6	1992	7	US-11-013-759-13
7	84	4.6	2047	7	US-11-013-759-4
8	84	4.6	2047	7	US-11-013-759-7
9	84	4.6	2053	7	US-11-013-759-9
10	83.5	4.6	585	1	US-10-510-386-20
11	83.5	4.6	594	1	US-10-510-386-38
12	83.5	4.6	721	7	US-11-060-920-5
13	81.5	4.5	543	1	US-10-495-664-3
14	81	4.4	348	1	US-10-793-626-2866
15	79	4.3	334	1	US-10-802-796-728
16	79	4.3	444	7	US-11-074-176-170
17	78	4.3	259	1	US-10-510-386-108
18	76.5	4.2	251	7	US-11-054-515-1833
19	75	4.1	249	7	US-11-054-515-1753
20	75	4.1	524	7	US-11-082-389-10
21	73	4.0	1213	7	US-11-074-176-256
22	72.5	4.0	643	1	US-10-510-386-8
23	72	3.9	227	1	US-10-858-730-86
24	72	3.9	835	1	US-10-501-039-4
25	71.5	3.9	80	1	US-10-821-234-949

ALIGNMENTS

RESULT 1

US-10-858-730-227  
; Sequence 227, Application US/10858730  
; Publication No. US2005025568A1  
; GENERAL INFORMATION:  
; APPLICANT: Bailey, Richard B.  
; APPLICANT: Blomquist, Paul  
; APPLICANT: Doten, Reed  
; APPLICANT: Driggers, Edward M.  
; APPLICANT: Madden, Kevin T.  
; APPLICANT: O'Leary, Jessica  
; APPLICANT: O'Toole, George  
; APPLICANT: Trueheart, Joshua  
; APPLICANT: Walbridge, Michael J.  
; APPLICANT: Yorgey, Peter S.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID  
; TITLE OF INVENTION: PRODUCTION  
; FILE REFERENCE: 14184-030001  
; CURRENT APPLICATION NUMBER: US/10/858,730  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/475,000  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: US 60/551,860  
; PRIOR FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 227  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-858-730-227

Query Match 5.2%; Score 94; DB 1; Length 417;  
Best Local Similarity 22.7%; Pred. No. 0.18;  
Matches 66; Conservative 34; Mismatches 115; Indels 76; Gaps 13;

QY	59	VNPYLGFEGYDNLGRMAYKGSVDNGAFKAGVOLTKALGYPITDDLDIVYTRLCGMVWRA	118
DB	93	VOPHSGSQANFAVYATLLEPGDTVLGMNLAHGHLTH--GSPVNFSGKLYNI---VPYGI	147
QY	119	DSKG--NYASTGVSRSEHD-----TGVSVPFAGGVEWAVTRDIATRL--EYOMVNNIGDAGT	171
DB	148	DATGHIDYADLEKQAKEHKPKMIIGGFSAYSGVDWAKMREIADSTGAYLFDVDMHVAVL	207
QY	172	VGTRPDNGMLSLGVSVRFQGEDAAPVAVAPAPAPAPV--ATKHFTLKSDVLPFNKATLK	229
DB	208	V-----AGVYPNPVPHAVVTTTTHKTLAG-----	233

Query Match 5.1%; Score 93; DB 1; Length 410;  
Best Local Similarity 20.4%; Pred. No. 0.22;

QY 215 LKSDVL--FNFNFKATLKPEQQALDQLYT---QLS-----NMDPKDGSVAVLGYTDR 261  
Db 262 IRLRLNGSNARDNLKLSNNQSFVYASDGGQLKNAKKLKTNLAPSERKEIVDLKSM 321  
QY 262 IGSE-----AYNQOLSEKRAQSVVDYLKAGIPAGKISARGHGESNPTGNT 308  
Db 322 KGEKISLVNDKTVILPISNKEKSNKGNTP---KVSQ-----KILEGMDNVDINGNK 373  
QY 309 CD 310  
Db 374 FD 375

RESULT 5

US-11-013-759-3  
Sequence 3, Application US/11013759  
Publication No. US20050249747A1  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
APPLICANT: Sasaki, Ken  
APPLICANT: Yang, Yan Ping  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
FILE REFERENCE: 1038-921MIS:jb  
CURRENT APPLICATION NUMBER: US/11/013,759  
CURRENT FILING DATE: 2004-12-16  
PRIOR APPLICATION NUMBER: US/09/361,619  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1992  
TYPE: PRT  
ORGANISM: Moraxella catarrhalis  
US-11-013-759-3

Query Match 4.6%; Score 84; DB 7; Length 1992;  
Best Local Similarity 20.1%; Pred. No. 11;  
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;  
QY 18 AGKLGWSQVHDTGYGNGFQNNNGPTRNDQLGAGA----FGGYQVNPYLG-----FEM 67  
Db 959 SGLKAGKSTLNDGGL-----SIKNPTGSEIQVGADGVKFAKVNNGVVGAGIDGTTRI 1012  
QY 68 GYDWLGRMAYKGSVDNG-----AFKAQGVQLT-AKLGYPTDDLDIYTRLGGMVWR-- 117  
Db 1013 TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKITTNIQSGEIAQNSHDAVT--GGKIYDLK 1070  
QY 118 -----ADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDI 154  
Db 1071 TELENKISSAKTAQNSLHFEVSADGQNNFTVSNPYSSYDT-----SKTSDV 1118  
QY 155 ATRLEYQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAAPVAPAPAPAEVATKHFT 214  
Db 1119 IT-----FAGENG-ITTKVKNKGVVRVGIQDTKG-----LTPKLTGVNNN 1157  
QY 215 LKSDVLNFKATLKPEQQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNQOLSEK 274  
Db 1158 GRGIVIDSQN-----GQNTITGLSNTLANVTNDRKGSVRTTEQGNIIKDE-----DKT 1204  
QY 275 RAQSVVDYLKAGIPAGKISARGHGES-----NPVTGNTC-----DNVKARAA 317  
Db 1205 RAASIVDVLSA-----GFNLQNGEAVDFVSTYDTVNFADGNATTAKVYDDTSTSKV 1258  
QY 318 LIDCLAPDRRVEIEVK--GYKEVVTOPAG 344  
Db 1259 VYDNNVDDTTIEVKDKKLGKVTTLTSTG 1287

RESULT 6

US-11-013-759-13

Sequence 13, Application US/11013759  
Publication No. US20050249747A1  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
APPLICANT: Sasaki, Ken  
APPLICANT: Yang, Yan Ping  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
FILE REFERENCE: 1038-921MIS:jb  
CURRENT APPLICATION NUMBER: US/11/013,759  
CURRENT FILING DATE: 2004-12-16  
PRIOR APPLICATION NUMBER: US/09/361,619  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 1992  
TYPE: PRT  
ORGANISM: Moraxella catarrhalis  
US-11-013-759-13

Query Match 4.6%; Score 84; DB 7; Length 1992;  
Best Local Similarity 20.1%; Pred. No. 11;  
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;  
QY 18 AGKLGWSQVHDTGYGNGFQNNNGPTRNDQLGAGA----FGGYQVNPYLG-----FEM 67  
Db 959 SGLKAGKSTLNDGGL-----SIKNPTGSEIQVGADGVKFAKVNNGVVGAGIDGTTRI 1012  
QY 68 GYDWLGRMAYKGSVDNG-----AFKAQGVQLT-AKLGYPTDDLDIYTRLGGMVWR-- 117  
Db 1013 TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKITTNIQSGEIAQNSHDAVT--GGKIYDLK 1070  
QY 118 -----ADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDI 154  
Db 1071 TELENKISSAKTAQNSLHFEVSADGQNNFTVSNPYSSYDT-----SKTSDV 1118  
QY 155 ATRLEYQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAAPVAPAPAPAEVATKHFT 214  
Db 1119 IT-----FAGENG-ITTKVKNKGVVRVGIQDTKG-----LTPKLTGVNNN 1157  
QY 215 LKSDVLNFKATLKPEQQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNQOLSEK 274  
Db 1158 GRGIVIDSQN-----GQNTITGLSNTLANVTNDRKGSVRTTEQGNIIKDE-----DKT 1204  
QY 275 RAQSVVDYLKAGIPAGKISARGHGES-----NPVTGNTC-----DNVKARAA 317  
Db 1205 RAASIVDVLSA-----GFNLQNGEAVDFVSTYDTVNFADGNATTAKVYDDTSTSKV 1258  
QY 318 LIDCLAPDRRVEIEVK--GYKEVVTOPAG 344  
Db 1259 VYDNNVDDTTIEVKDKKLGKVTTLTSTG 1287

RESULT 7

US-11-013-759-4  
Sequence 4, Application US/11013759  
Publication No. US20050249747A1  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
APPLICANT: Sasaki, Ken  
APPLICANT: Yang, Yan Ping  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
FILE REFERENCE: 1038-921MIS:jb  
CURRENT APPLICATION NUMBER: US/11/013,759  
CURRENT FILING DATE: 2004-12-16  
PRIOR APPLICATION NUMBER: US/09/361,619  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1



Db 1280 GFNLQNGEAVDFVSTVDTNFGANGTTAKTVYDDTSKTSKVYVDVNDVDDTTTIEVKDKK 1339

Qy 334 -GYKEVVTPAG 344

Db 1340 LGVKTTLTSTG 1351

## RESULT 10

US-10-510-386-20  
; Sequence 20, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olsen, Peter Bjarke  
; APPLICANT: Rasmussen, Michael Dolberg  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10294.204-US  
; CURRENT APPLICATION NUMBER: US/10/510,386  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; TYPE: PRT  
; ORGANISM: Bacillus licheniformis  
US-10-510-386-20

Query Match 4.6%; Score 83.5; DB 1; Length 585;

Best Local Similarity 26.1%; Pred. No. 2.4;  
Matches 52; Conservative 20; Mismatches 70; Indels 57; Gaps 11;

Qy 98 GYPITDLDIYTLGCMVWRADSKGNVASTGVRSEHDTGCVSPVAGGVEMAVTRDIATR 157

Db 382 GYPVLDREGWGLR-NLFSAADGYGAF-----TKNVTVTMDSAKGGFH---TAD----- 426

Qy 158 LEYQWNNIGDAGTV-----GTRPDNGMLSLGVSYRFGQSDAA--PV 197

Db 427 ---RWENDISGTGKTKKGTGALKLEGDNNTYSGTRIDQGTLEGGSETAFGRGDVALNGG 483

Qy 198 VAPAPAP-----APEVATKHTLKSDVLFNFNFKATLKPEGQOALDOLYTOLSN 245

Db 484 ILKEDAPGKLIIEGDYKQSAKGILEQLSGKKDQIKKGKARLK--GTLRLN--FT--DN 537

Qy 246 MDPKGSAAVLGYTDRIGS 264

Db 538 YVPADGSAIIT-FRKRHGS 555

## RESULT 11

US-10-510-386-38  
; Sequence 38, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olsen, Peter Bjarke  
; APPLICANT: Rasmussen, Michael Dolberg  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10294.204-US  
; CURRENT APPLICATION NUMBER: US/10/510,386  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 38  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Bacillus licheniformis  
US-10-510-386-38

Query Match 4.6%; Score 83.5; DB 1; Length 594;

Best Local Similarity 26.1%; Pred. No. 2.4;  
Matches 52; Conservative 20; Mismatches 70; Indels 57; Gaps 11;

Qy 98 GYPITDLDIYTLGCMVWRADSKGNVASTGVRSEHDTGCVSPVAGGVEMAVTRDIATR 157

Db 387 GYPVLDREGWGLR-NLFSAADGYGAF-----TKNVTVTMDSAKGGFH---TAD----- 431

Qy 158 LEYQWNNIGDAGTV-----GTRPDNGMLSLGVSYRFGQSDAA--PV 197

Db 432 ---RWENDISGTGKTKKGTGALKLEGDNNTYSGTRIDQGTLEGGSETAFGRGDVALNGG 488

Qy 198 VAPAPAP-----APEVATKHTLKSDVLFNFNFKATLKPEGQOALDOLYTOLSN 245

Db 489 ILKEDAPGKLIIEGDYKQSAKGILEQLSGKKDQIKKGKARLK--GTLRLN--FT--DN 542

Qy 246 MDPKGSAAVLGYTDRIGS 264

Db 543 YVPADGSAIIT-FRKRHGS 560

## RESULT 12

US-11-060-920-5  
; Sequence 5, Application US/11060920  
; Publication No. US20050244378A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaufman, Paul L  
; APPLICANT: Liu, Xuyang  
; TITLE OF INVENTION: Method for Treating Glaucoma  
; FILE REFERENCE: 960296.00149  
; CURRENT APPLICATION NUMBER: US/11/060,920  
; CURRENT FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: US 60/545,723  
; PRIOR FILING DATE: 2004-02-18  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 721  
; TYPE: PRT  
; ORGANISM: Clostridium botulinum  
US-11-060-920-5

Query Match 4.6%; Score 83.5; DB 7; Length 721;

Best Local Similarity 20.9%; Pred. No. 3.1;  
Matches 71; Conservative 39; Mismatches 117; Indels 113; Gaps 17;

Qy 2 KAIFVLNAAPKDNWTYAGGKLGWSQYHDTGFGV-----NGF--ONNNGPTRNDQLGAG 52

Db 165 KSKFIPN-----NTLFSNAKLKANANRDTDRDGPDEWEINGYTMVNOKAVAMDDKFAAN 219

Qy 53 AFGGYQVN-----PYLGFEMGYDWLGRMAYKGSVDN-----GAFKAQGVQ 92

Db 220 GYKKVSNPFKPECTANDPYTDFE-----KVSQIDPSVSMVARDPMISAYPIVGVO 270

Qy 93 ---LTAKLGPITDLDIYTLGCMVWRADSKG-NYASTGCVSRSEHDTGVPVAGGVEM 148

Db 271 MERLVVSKSETITGDST-----KSMKSTSHSNTINTVGAESVSLQLAGIIP 320

Qy 149 AVTRDIATRLFYQWNNIGDAGTVGTRPDNGM-LSLGVS-----YRFGQEDAAPVAPA 201

Db 321 VFSMSASANSYHTWNTSTVDDTTGESPQGLSINTGESAYINPNIRYNTGTAPVYNT 380

Qy 202 PAPAPEVATKHTLKSDVLFNFNFKATLKPEGQOAL-----D 237

Db 381 PT-----TTIVDKOSVATIK--GQSLIGDYLNPGGTYPIIGEPPTMALNTMD 426

Qy 238 QL-----YTQLSNMDPKGSAAVLGYTDRIGSEA--YN 268

Db 427 QFSSRLIPYNQLKSID--NGGTWMLSTSQFTGNPAKYN 464

## RESULT 13

US-10-495-664-3  
; Sequence 3, Application US/10495664

Publication No. US20050244416A1  
; GENERAL INFORMATION:  
; APPLICANT: JUNG, GUNDRAM  
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE  
; FILE REFERENCE: 034258-0801  
; CURRENT APPLICATION NUMBER: US/10/495,664  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: PCT/EP02/12545  
; PRIOR FILING DATE: 2002-11-09  
; PRIOR APPLICATION NUMBER: DE 101 56 482.1  
; PRIOR FILING DATE: 2001-11-12  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent In Ver. 3.3  
; SEQ ID NO 3  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: protein construct  
US-10-495-664-3

Query Match 4.5%; Score 81.5; DB 1; Length 543;  
Best Local Similarity 20.8%; Pred. No. 3.2;  
Matches 64; Conservative 42; Mismatches 121; Indels 81; Gaps 15;  
QY 7 LNAAPKDNNT--WYAGGKLGHSQYHDTGFYCGNG-----FQNNNGPT-----RNDQLGAGAF 54  
DB 229 MNSLQADDTAVVYCARDKGYSYYYDMYQGQTTVTSSASTXGSPVFPPLAPSSSGSQV 288  
QY 55 GGYQVNPYL-----GFE-----MGYDVLGRMAYKGSVD--N 83  
DB 289 KLOQSGPELVKPGASVKISKASGAYFASRWMMWVQKPCQGLEWIGRI-YPGDGTNTYN 347  
QY 84 GAFKAQGVOLTA-----KLGYPTDLDIYTRLGG-----MWRADSKGNVASTGVS 130  
DB 348 GKFKGKAT-LTADKSSSTAYMQVSSLTSDSAVYFCARGNTVVVPTMDYWGQGTIVTVS 406  
QY 131 RSEHDTGVSVPFAGGVEWATRIATRLLEYQWNNITGDAGTGTTRPDNGMLSLGVSYR-- 188  
DB 407 SGGGGGGGGGGGGSDIELTQSPAS-----LAVSLGQRATISCRASESDSYGNSFMHW 461  
QY 189 FGQEDAAPVAPAPAPAPAPAPVATKHTLTKSDVLFNFNKA-----TLKPEGQQAALDQLY 240  
DB 462 YQKPKQCP-----PKLLIYLAS---NLESGVPARFSGSGSRDTFTLTIDPVEADDAATY 513  
QY 241 TQLSNMDP 248  
DB 514 CQONNEDP 521

RESULT 14  
US-10-793-626-2866  
; Sequence 2866, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2866  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2866

Query Match 4.4%; Score 81; DB 1; Length 348;  
Best Local Similarity 20.9%; Pred. No. 2;  
Matches 77; Conservative 41; Mismatches 90; Indels 160; Gaps 22;  
QY 12 KONTWAGKLGWSQYHDTGFYCGNGFQNNNGPTNRNDQLGAGAFGGYQVNPYLGFMG 68  
DB 75 KDNNGYKNYTLK-AQEGKTEFYKNNFSNTLG-----YNGNLLGPTLKLKGDVKV 122  
QY 69 -----YDWLGRMAYKGSVDNG-----AFKAQGVQVLTAKLGY----- 99  
DB 123 KIKLINLNDENTTFHWHG-LEVNGKYVDGSPQVIRKPEKKTIKFEYNQDSATLWYHPHPS 181  
QY 100 PITDDLDIYTRLGGMWRADS-KGNVASTGVSRSSEHDTGSPVFAAGGVEMAVTRD--IA 155  
DB 182 PNTAK-QVYNGLSGLYIETDSKKNYP-----SDYGRKNDLFI-----IIQDKTFVS 226  
QY 156 TRLEYQWNNIGDAGTVG-TRPDNGMLSLGVSYRFQGEDAAPVAPAPAPAPAPAPVATKHPT 214  
DB 227 KKLNYSKTKD--EDGTQGDVTLVNGIVN-----PKLTTKEEK 261  
QY 215 LKSDVLFNFNKAATLKPEGQQAALDQLYTQLSNMDPKDGSVAVLYGTYDRIGSEAYNQOLSEK 274  
DB 262 IRLRLT-----NGSNARD-LNLKLSN-----NQSF--- 285  
QY 275 RAQSVVDVYLVAKGIPAGKI-SARGHGESNPVTGNTCDNVKARAALDCLAPDRRVEI--- 330  
DB 286 -----EYASDG---GQLKNAKLUKEIN-----LAPSRKEIVID 317  
QY 331 --EVKGK 336  
DB 318 LSKMKGEK 325

RESULT 15  
US-10-802-796-728  
; Sequence 728, Application US/10802796  
; Publication No. US20050250104A1  
; GENERAL INFORMATION:  
; APPLICANT: COLE, STEWART  
; APPLICANT: BUCHRIESER-BROSCH, ROLAND  
; APPLICANT: GORDON, STEPHEN  
; APPLICANT: BILLAULT, ALAIN  
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST  
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC BASED  
; TITLE OF INVENTION: DNA LIBRARY.  
; FILE REFERENCE: 05394.0011-00000  
; CURRENT APPLICATION NUMBER: US/10/802,796  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/673,476  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: PCT/IB99/00740  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 09/060,756  
; PRIOR FILING DATE: 1998-04-16  
; NUMBER OF SEQ ID NOS: 743  
; SOFTWARE: Patent In Ver. 2.2  
; SEQ ID NO 728  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Mycobacterium sp.  
US-10-802-796-728

Query Match 4.3%; Score 79; DB 1; Length 334;  
Best Local Similarity 26.0%; Pred. No. 2.8;  
Matches 44; Conservative 11; Mismatches 56; Indels 58; Gaps 8;  
QY 18 AGGKLGWSQYHDTGFY-GNGFQNNNGPTNRNDQLGAGAFGGYQVNPYLGFMG-YDWLGRM 75  
DB 187 AGGAGGF-----GFLGGDGGAGNAGLLSSGGGFGGFGTAGVGGAGNAGWLGFG 240  
QY 76 A-----YKGSVDNAGAFKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKGNVASTGVS 130



Db	241	AGGIGGIGNANGGAGNGGT-----GGQWGGGAG--VEGAA	278
Qy	131	RSEHDTGVSFVFAGGVEMAVTRDIATFLEYQWVNNIGDAGTVGTRPDNG	179
Db	279	LSVGD TG-----GAGGVG-----GSAGLIGTGNGG	304

Search completed: November 26, 2005, 00:21:22  
Job time : 11 secs

**This Page Blank (usp10)**







Best Local Similarity 82.8%; Pred. No. 1.8e-130;  
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;  
QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65  
DB 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72  
QY 66 EMGYDMLGRMAYKGSVDNGAFKAGQVLTAKLGYPITDLDIYTRLGGMWVRADSKGNYA 125  
DB 73 EMGYDMLGRMPYKGDNTNGAYKAGQVLTAKLGYPITDLDIYTRLGGMWVRADTSKNVP 132  
QY 126 STGVSSEHDTGVSVPFAGGVEAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGV 185  
DB 133 G-CASTKHDTGVSVPFAGGIEVAITPEIATRLLEYQVNNIGDANTIGTRPDNGLLSVGV 191  
QY 186 SYRFGQEDAAPVAP 245  
DB 192 SYRFGQEDAAPVAP 251  
QY 246 MDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305  
DB 252 LDPKGSAAVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311  
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342  
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 348

RESULT 8  
US-10-946-647-1389  
; Sequence 1389, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, DARYLL A.  
; APPLICANT: STRAUB, DARREN E.  
; APPLICANT: WONDERLING, LAURA  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; PRIOR FILING DATE: 2004-09-20  
; PRIOR FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1389  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Salmonella enterica  
US-10-946-647-1389

Query Match 82.0%; Score 1495; DB 5; Length 350;  
Best Local Similarity 82.8%; Pred. No. 4.1e-130;  
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;  
QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65  
DB 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72  
QY 66 EMGYDMLGRMAYKGSVDNGAFKAGQVLTAKLGYPITDLDIYTRLGGMWVRADSKGNYA 125  
DB 73 EMGYDMLGRMPYKGDNTNGAYKAGQVLTAKLGYPITDLDIYTRLGGMWVRADTSKNVP 132  
QY 126 STGVSSEHDTGVSVPFAGGVEAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGV 185  
DB 133 G-GPSTKHDTGVSVPFAGGIEVAITPEIATRLLEYQVNNIGDANTIGTRPDNGLLSVGV 191  
QY 186 SYRFGQEDAAPVAP 245  
DB 192 SYRFGQEDAAPVAP 251  
QY 246 MDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305  
DB 252 LDPKGSAAVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311

QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342  
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 348  
RESULT 9  
US-10-946-647-1395  
; Sequence 1395, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, DARYLL A.  
; APPLICANT: STRAUB, DARREN E.  
; APPLICANT: WONDERLING, LAURA  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; CURRENT FILING DATE: 2004-09-20  
; PRIOR FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1395  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Salmonella enterica  
US-10-946-647-1395

Query Match 82.0%; Score 1495; DB 5; Length 350;  
Best Local Similarity 82.8%; Pred. No. 4.1e-130;  
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;  
QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65  
DB 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72  
QY 66 EMGYDMLGRMAYKGSVDNGAFKAGQVLTAKLGYPITDLDIYTRLGGMWVRADSKGNYA 125  
DB 73 EMGYDMLGRMPYKGDNTNGAYKAGQVLTAKLGYPITDLDIYTRLGGMWVRADTSKNVP 132  
QY 126 STGVSSEHDTGVSVPFAGGVEAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGV 185  
DB 133 G-GPSTKHDTGVSVPFAGGIEVAITPEIATRLLEYQVNNIGDANTIGTRPDNGLLSVGV 191  
QY 186 SYRFGQEDAAPVAP 245  
DB 192 SYRFGQEDAAPVAP 251  
QY 246 MDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305  
DB 252 LDPKGSAAVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311  
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342  
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 348

RESULT 10  
US-10-946-647-1404  
; Sequence 1404, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, DARYLL A.  
; APPLICANT: STRAUB, DARREN E.  
; APPLICANT: WONDERLING, LAURA  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; CURRENT FILING DATE: 2004-09-20  
; PRIOR FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1404  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Salmonella enterica  
US-10-946-647-1404

Query Match 82.0%; Score 1495; DB 5; Length 350;  
Best Local Similarity 82.8%; Pred. No. 4.1e-130;  
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;  
  
QY 6 VLNAAPKDNWTYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPVYLG 65  
Db 18 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPVYGF 72  
  
QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125  
73 EMGYDWLGRMPYKGDNINGAYKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKSNP 132  
  
QY 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 185  
Db 133 G-GPSTKDHDTGVSVPFAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 191  
  
QY 186 SYRFGQSDRAAPVAP 245  
Db 192 SYRFGQSDRAAPVAP 251  
  
QY 246 MDPKDGSAVVLGYTDRIGSAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305  
Db 252 LDPKDGSAVVLGYTDRIGSAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311  
  
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGKVVQTP 342  
Db 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGKVVQTP 348

## RESULT 11

US-10-416-708A-24  
; Sequence 24, Application US/10416708A  
; Publication No. US20040161753A1  
; GENERAL INFORMATION:

; APPLICANT: Wise, John G.  
; APPLICANT: Fromknecht, Katja  
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
; FILE REFERENCE: 37779-0004  
; CURRENT APPLICATION NUMBER: US/10/416,708A  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 24  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-416-708A-24

Query Match 41.4%; Score 754; DB 4; Length 190;  
Best Local Similarity 79.9%; Pred. No. 1.3e-61;  
Matches 139; Conservative 9; Mismatches 16; Indels 10; Gaps 2;  
  
QY 6 VLNAAPKDNWTYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPVYLG 65  
Db 20 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPVYGF 74  
  
QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125  
Db 75 EMGYDWLGRMPYKGSVENGAYKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKSN-- 132  
  
QY 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 179  
Db 133 ---VYGNKDHDTGVSVPFAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 183

## RESULT 12

US-10-416-708A-27  
; Sequence 27, Application US/10416708A  
; Publication No. US20040161753A1  
; GENERAL INFORMATION:

; APPLICANT: Wise, John G.  
; APPLICANT: Fromknecht, Katja  
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
; FILE REFERENCE: 37779-0004  
; CURRENT APPLICATION NUMBER: US/10/416,708A  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 27  
; LENGTH: 192  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-416-708A-27

Query Match 41.4%; Score 754; DB 4; Length 192;  
Best Local Similarity 79.9%; Pred. No. 1.3e-61;  
Matches 139; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPVYLG 65  
Db 20 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPVYGF 74  
  
QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125  
Db 75 EMGYDWLGRMPYKGSVENGAYKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKSN-- 132  
  
QY 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 179  
Db 133 ---VYGNKDHDTGVSVPFAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 183

## RESULT 13

US-10-416-708A-10  
; Sequence 10, Application US/10416708A  
; Publication No. US20040161753A1  
; GENERAL INFORMATION:

; APPLICANT: Wise, John G.  
; APPLICANT: Fromknecht, Katja  
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
; FILE REFERENCE: 37779-0004  
; CURRENT APPLICATION NUMBER: US/10/416,708A  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 10  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-416-708A-10

Query Match 41.0%; Score 748; DB 4; Length 194;  
Best Local Similarity 79.8%; Pred. No. 4.9e-61;  
Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPVYLG 65  
Db 20 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPVYGF 74  
  
QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125  
Db 75 EMGYDWLGRMPYKGSVENGAYKAQGVQVLTAKLGYPTDLDIYTRLGGMWRADSKSN-- 132





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:50:22 ; Search time 188 Seconds  
(without alignments)  
803.970 Million cell updates/sec

Title: US-09-913-772a-2

Perfect score: 1823

Sequence: 1 MKAFVINAAPKONTWYAGS.....DRVEIEVKGYKEVVTQPAG 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1823	100.0	344	3	AAB18994 A P40 pol
2	1823	100.0	344	3	AAB08317 An outer
3	1823	100.0	344	3	AAY93341 Amino aci
4	1823	100.0	344	3	AAB08825 A P40 pol
5	1823	100.0	344	3	AAB18804 A Klebsie
6	1823	100.0	344	3	AAB08341 An outer
7	1823	100.0	344	3	AAG63698 Amino aci
8	1823	100.0	344	4	AAB67770 Amino aci
9	1823	100.0	344	5	AAM48395 Klebsiell
10	1823	100.0	344	5	AAM47796 Klebsiell
11	1823	100.0	344	8	ADI00532 Klebsiell
12	1823	100.0	344	8	ADI56807 K. pneumo
13	1823	100.0	344	8	ADI38366 K. pneumo
14	1818	99.7	344	2	AAR93797 Protein L
15	1818	99.7	452	4	AAB67771 Amino aci
16	1813	99.5	344	2	AAY44077 K.pneumon
17	1813	99.5	344	4	AAG67743 Amino aci
18	1813	99.5	344	4	AAB84122 Amino aci
19	1782	97.8	385	7	ABO60934 Klebsiell
20	1781	97.7	335	2	AAR88257 K.pneumon
21	1781	97.7	335	2	AAR95644 Klebsiell
22	1781	97.7	335	2	AAR93796 Protein P
23	1289	70.7	369	6	ABM69278 Phototrab
24	1279	70.2	384	7	ADF07637 Bacterial

25	1026	56.3	188	2	AAR93798	Aar93798 Protein L
26	984	54.0	179	2	AAR95645	Aar95645 Klebsiell
27	689	37.8	344	5	AAM50724	Aam50724 Haemophil
28	688	37.7	344	5	AAM50721	Aam50721 Haemophil
29	687	37.7	137	5	ABB83156	Abb83156 Partial O
30	687	37.7	153	5	AAE17872	AAe17872 Sequence
31	685	37.6	344	5	AAM50718	Aam50718 Haemophil
32	684	37.5	344	5	AAM50719	Aam50719 Haemophil
33	684	37.5	344	5	AAM50717	Aam50717 Haemophil
34	684	37.5	344	5	AAM50716	Aam50716 Haemophil
35	684	37.5	344	5	AAM50722	Aam50722 Haemophil
36	683	37.5	344	5	AAM50725	Aam50725 Haemophil
37	680.5	37.3	341	5	AAM50720	Aam50720 Haemophil
38	680.5	37.3	341	5	AAM50723	Aam50723 Haemophil
39	680.5	37.3	341	5	AAM50726	Aam50726 Haemophil
40	678	37.2	344	5	AAM50727	Aam50727 Haemophil
41	671	36.8	364	3	AAB44588	Aab44588 Virulence
42	671	36.8	364	3	ABP54540	Abp54540 Actinobac
43	667	36.6	364	3	AAY97899	Aay97899 Actinobac
44	667	36.6	364	3	AAY96097	Aay96097 Actinobac
45	655.5	36.0	359	2	AAR66294	Aar66294 Non-typab

#### ALIGNMENTS

#### RESULT 1

AAB18994  
ID AAB18994 standard; protein; 344 AA.  
XX  
AC AAB18994;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE A P40 polypeptide of Klebsiella pneumoniae.

XX P40; membrane fraction; Gram-negative bacteria; anticancer;  
XX immune response; mononuclear blood cell; tumour necrosis factor-alpha;  
XX interleukin-12; antitumour; cancer.

OS Klebsiella pneumoniae.

XX WO2000054790-A1.

PN 21-SEP-2000.

XX 15-MAR-2000; 2000WO-FR000623.

PR 15-MAR-1999; 99FR-00003154.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Libon C, Corvaia N, Beck A, Bonnefoy J;

XX WPI; 2000-587477/55.

XX N-PSDB; AAA96568.

XX Use of membrane fractions from Gram-negative bacteria as immunostimulants  
XX for the treatment or prevention of cancer, increases effect of e.g.  
XX chemotherapeutic agents.

XX Claim 6; Page 27-28; 34pp; French.

XX The present sequence represents a P40 polypeptide of Klebsiella  
XX pneumoniae. The protein is found in the membrane fraction, and is used in  
XX the method of the invention. The specification describes the use of a  
XX membrane fraction from Gram-negative bacteria for the preparation of an  
XX immunostimulating composition that can induce an anticancer immune  
XX response. The membrane fraction not only stimulates proliferation of  
XX human mononuclear blood cells (immunostimulation) but also induces  
XX production of tumour necrosis factor-alpha and interleukin (IL)-12, which  
XX are known to have antitumour activity, so that it improves the effects of  
XX other co-administered anticancer treatments (chemotherapy or radiation).

















S. enteritidis, S. panama and S. dublin. A vaccine prepared using an oligosaccharide from S. enteritidis can be used to provide protection against septicaemia caused by S. typhi and against typhoid fever, as well as to protect humans and animals from toxic infections and zoonosis caused by Salmonella of the same serogroup. The carrier proteins enhance the immunogenicity of the oligo- or polysaccharide antigens. Inclusion of additional Salmonella capsule antigens, such as the Vi antigen, increases the vaccine's efficacy against encapsulated bacteria. The present sequence, protein LP40, is a preferred example of a carrier protein which can be used in the immunocomplex. It is obtained by recombinant expression of a modified kieb. pneumoniae I-145 P40 gene in E. coli

[illegible]

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**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 00:03:28 ; Search time 46 Seconds  
(without alignments)  
618.270 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVLNAPKDNWTYAGG.....DRVEIEVKGYKEVVTQPA 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PGTUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1782	97.8	385	2	US-09-489-039A-7451
2	1781	97.7	335	2	US-08-836-500A-2
3	1781	97.7	335	2	US-09-679-750-2
4	1279	70.2	384	2	US-09-543-681A-7922
5	984	54.0	179	2	US-08-836-500A-4
6	984	54.0	179	2	US-09-679-750-4
7	671	36.8	364	2	US-09-809-665A-151
8	667	36.6	364	2	US-09-418-980-8
9	667	36.6	364	2	US-09-506-078-45
10	662.5	36.3	359	1	US-08-457-997B-2
11	662.5	36.3	359	2	US-08-467-722A-2
12	662.5	36.3	359	2	US-09-451-184-2
13	646.5	35.5	369	2	US-09-809-665A-153
14	639.5	35.1	369	2	US-09-418-980-10
15	639.5	35.1	369	2	US-09-506-078-46
16	586.5	32.2	338	1	US-08-210-394-1
17	379	20.8	72	2	US-08-836-500A-6
18	379	20.8	72	2	US-09-679-750-6
19	281	15.4	53	2	US-08-836-500A-8
20	281	15.4	53	2	US-09-679-750-8
21	242.5	13.3	379	2	US-09-328-352-5219
22	231.5	12.7	351	2	US-09-252-991A-30094
23	224.5	12.3	349	2	US-09-573-630A-2
24	200	11.0	342	2	US-09-902-540-15847
25	199	10.9	235	2	US-09-252-991A-19595
26	193.5	10.6	259	2	US-09-328-352-5775
27	184.5	10.1	566	2	US-09-489-039A-14179

28	182	10.0	220	2	US-09-489-039A-11012	Sequence 11012, A
29	182	10.0	226	1	US-08-572-447C-15	Sequence 15, Appl
30	182	10.0	226	2	US-09-267-747-15	Sequence 15, Appl
31	181	9.9	161	1	US-08-572-447C-11	Sequence 11, Appl
32	181	9.9	161	2	US-09-267-747-11	Sequence 11, Appl
33	176.5	9.7	266	2	US-09-252-991A-18046	Sequence 18046, A
34	175	9.6	633	2	US-09-489-039A-13729	Sequence 13729, A
35	175	9.6	753	2	US-09-252-991A-17612	Sequence 17612, A
36	170	9.3	472	2	US-09-328-352-6870	Sequence 6870, Ap
37	169.5	9.3	272	2	US-09-252-991A-29681	Sequence 29681, A
38	168.5	9.2	214	1	US-08-572-447C-13	Sequence 13, Appl
39	168.5	9.2	214	2	US-09-267-747-13	Sequence 13, Appl
40	168	9.2	409	2	US-09-902-540-12745	Sequence 12745, A
41	167.5	9.1	344	2	US-09-902-540-12463	Sequence 12463, A
42	165.5	9.1	417	2	US-09-252-991A-26245	Sequence 26245, A
43	163.5	9.0	169	2	US-09-252-991A-19373	Sequence 19373, A
44	161	8.8	278	2	US-09-328-352-5824	Sequence 5824, Ap
45	158	8.7	257	2	US-09-328-352-6621	Sequence 6621, Ap

ALIGNMENTS

RESULT 1  
US-09-489-039A-7451  
; Sequence 7451, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLBBSIELLA  
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 7451  
; LENGTH: 385  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7451

Query Match	97.8%;	Score 1782;	DB 2;	Length 385;
Best Local Similarity	99.4%;	Pred. No. 4.3e-169;		
Matches 336;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	6	VLNAAPKDNTWAGGKLGWSQYHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVNPYLG	65	
Db	47	VAQAAPKDNTWAGGKLGWSQYHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVNPYLG	106	
QY	66	EMGYDMLGRMAKGSVDNGAFKAQGVQLTAKLGYPTDDLDIYTRLGGMWVRADSKGNYA	125	
Db	107	EMGYDMLGRMAKGSVDNGAFKAQGVQLTAKLGYPTDDLDIYTRLGGMWVRADSKGNYA	166	
QY	126	STGVSRSEHDTGVSVPFAGGVWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV	185	
Db	167	STGVSRSEHDTGVSVPFAGGVWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV	226	
QY	186	SYRFGQEDAAPVAPAPAPAPVATKHFTLKSVDLNFNFNKATLKPEGQALDQLYTOLSN	245	
Db	227	SYRFGQEDAAPVAPAPAPAPVATKHFTLKSVDLNFNFNKATLKPEGQALDQLYTOLSN	286	
QY	246	MDPKDGSVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT	305	
Db	287	MDPKDGSVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT	346	
QY	306	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA	343	
Db	347	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA	384	

RESULT 2

RESULT 2

US-08-836-500A-2

/ Sequence 2, Application US/08836500A  
Patent No. 6197929

GENERAL INFORMATION:  
APPLICANT: Binz, Hans  
APPLICANT: Baussant, Thierry  
APPLICANT: Haeuw, Jean-Francois  
TITLE OF INVENTION: Carrier Protein Having an Adjuvant Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines

TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines

Patent No. 6197929

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.  
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,500A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
REFERENCE/DOCKET NUMBER: PIE1514P0180US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-500A-2

Query Match 97.7%; Score 1781; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.4e-169;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKNTWYAGGKLGSQYHDTGFYNGFNQNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69  
1 APKNTWYAGGKLGSQYHDTGFYNGFNQNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 60

Db 70 DWLGRMYKGSVDNMGAFKAQQVLTAKLGYPITDDLDIYTRLGMVMWRADSKGNVYSTGV 129  
61 DWLGRMYKGSVDNMGAFKAQQVLTAKLGYPITDDLDIYTRLGMVMWRADSKGNVYSTGV 120

Qy 130 SRSEHTGVSVPFAGGVEAVTTRDIATRLBYQVWNIGDAGTVGTTRPDNGLSLGVSYRF 189  
121 SRSEHTGVSVPFAGGVEAVTTRDIATRLBYQVWNIGDAGTVGTTRPDNGLSLGVSYRF 180

Db 190 QGEDAAPVAPAPAPAPEVATKHFTLKSDVLNFNKATLKPEGOALDOLYTOLSNMDPK 249  
181 QGEDAAPVAPAPAPAPEVATKHFTLKSDVLNFNKATLKPEGOALDOLYTOLSNMDPK 240

Qy 250 DGSVVLYGTYDRIGSEAYNQQLSEKRAQSVDYLVAKGIPACKISARGMGESNPVTGNTC 309  
241 DGSVVLYGTYDRIGSEAYNQQLSEKRAQSVDYLVAKGIPACKISARGMGESNPVTGNTC 300

Db 310 DNVKARAALIDCLAPRRRVEIEVKGEVVTQPAG 344  
301 DNVKARAALIDCLAPRRRVEIEVKGEVVTQPAG 335

US-08-836-500A-2

/ Sequence 2, Application US/08836500A  
Patent No. 6197929

GENERAL INFORMATION:  
APPLICANT: Binz, Hans  
APPLICANT: Baussant, Thierry  
APPLICANT: Haeuw, Jean-Francois  
TITLE OF INVENTION: Carrier Protein Having an Adjuvant Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines

TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines

Patent No. 6197929

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.  
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,500A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
REFERENCE/DOCKET NUMBER: PIE1514P0180US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-500A-2

Query Match 97.7%; Score 1781; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.4e-169;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKNTWYAGGKLGSQYHDTGFYNGFNQNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69  
1 APKNTWYAGGKLGSQYHDTGFYNGFNQNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 60

Db 70 DWLGRMYKGSVDNMGAFKAQQVLTAKLGYPITDDLDIYTRLGMVMWRADSKGNVYSTGV 129  
61 DWLGRMYKGSVDNMGAFKAQQVLTAKLGYPITDDLDIYTRLGMVMWRADSKGNVYSTGV 120

Qy 130 SRSEHTGVSVPFAGGVEAVTTRDIATRLBYQVWNIGDAGTVGTTRPDNGLSLGVSYRF 189  
121 SRSEHTGVSVPFAGGVEAVTTRDIATRLBYQVWNIGDAGTVGTTRPDNGLSLGVSYRF 180

Db 190 QGEDAAPVAPAPAPAPEVATKHFTLKSDVLNFNKATLKPEGOALDOLYTOLSNMDPK 249  
181 QGEDAAPVAPAPAPAPEVATKHFTLKSDVLNFNKATLKPEGOALDOLYTOLSNMDPK 240

Qy 250 DGSVVLYGTYDRIGSEAYNQQLSEKRAQSVDYLVAKGIPACKISARGMGESNPVTGNTC 309  
241 DGSVVLYGTYDRIGSEAYNQQLSEKRAQSVDYLVAKGIPACKISARGMGESNPVTGNTC 300

Db 310 DNVKARAALIDCLAPRRRVEIEVKGEVVTQPAG 344  
301 DNVKARAALIDCLAPRRRVEIEVKGEVVTQPAG 335

Db 241 DGSVAVLGYTDRIGSEAYNOOLSEKRAQSVVDYLVAKIPAGKISARGMGESNPVTGNTC 300  
Qy 310 DNKARAALIDCLAPDRRVEIEVKYKEVVTQAPG 344  
Db 301 DNKARAALIDCLAPDRRVEIEVKYKEVVTQAPG 335

RESULT 4  
US-09-543-681A-7922  
; Sequence 7922, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543.681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7922  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7922

Query Match 70.2%; Score 1279; DB 2; Length 384;  
Best Local Similarity 71.5%; Pred. No. 6.4e-119;  
Matches 243; Conservative 32; Mismatches 59; Indels 6; Gaps 3;

Qy 9 AAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYQVNPYLGPEMG 68  
Db 43 AAPKDNWTYGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYQVNPYLGPEMG 102  
Qy 69 YDWLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDLDIYTRLCGMVWRADSKG--NYAS 126  
Db 103 YDWLGRMAYKGSYNNAGAFKAGQVOLTAKLGYPTDLDIYTRLCGMVWRADSKG--NYAS 162  
Qy 127 TGVS--SEHDTGVSVPAGVSMVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLG 184  
Db 163 AGTKRFSNDTGVSPVAFALGTETATPNTATRLLEYQVNNIGDAGTVGTRPDNGMLSLG 222  
Qy 185 VSYRFGQEDAAPVAPAP--APAPEVATKHTLKSVDLFLNFENKATLKPEQQALDOLYTQ 242  
Db 223 VAYRFQETPAPVVEPAPVAPVVENKFTLRSDFVFNKSSLKAEQOEALNGLYNE 282  
Qy 243 LSNMOPKGSVAVLGYTDRIGSEAYNOOLSEKRAQSVVDYLVAKIPAGKISARGMGESN 302  
Db 283 LANIDPTQGRVWVIGYTDRTIGSQYNNPLSEKRAQSVVDYLVAKIPAGKISARGMGESN 342  
Qy 303 PVTGNTCDNKKARAALIDCLAPDRRVEIEVKYKEVVTQ 342  
Db 343 PVTGNTCDNKKARAALIDCLAPDRRVEIEVKYKEVVTQ 382

RESULT 5  
US-08-836-500A-4  
; Sequence 4, Application US/08836500A  
; Patent No. 6197929  
; GENERAL INFORMATION:  
; APPLICANT: Binz, Hans  
; APPLICANT: Baussant, Thierry  
; APPLICANT: Haeuw, Jean-Francois  
; APPLICANT: Nguyen Ngoc, Thien  
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant  
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for  
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines  
; Patent No. 6197929  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.  
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite

STREET: 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,500A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
REFERENCE/DOCKET NUMBER: PIB1514P0180US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-500A-4

Query Match 54.0%; Score 984; DB 2; Length 179;  
Best Local Similarity 100.0%; Pred. No. 5.4e-90;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYQVNPYLGPEMG 69  
Db 1 APKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYQVNPYLGPEMG 60  
Qy 70 DMLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDLDIYTRLCGMVWRADSKGNYASTGV 129  
Db 61 DMLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDLDIYTRLCGMVWRADSKGNYASTGV 120  
Qy 130 SRSEHDTGVSVPAGVSMVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGVSYSR 188  
Db 121 SRSEHDTGVSVPAGVSMVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGVSYSR 179

RESULT 6  
US-09-679-750-4  
; Sequence 4, Application US/09679750  
; Patent No. 6780420  
; GENERAL INFORMATION:  
; APPLICANT: Binz, Hans  
; APPLICANT: Baussant, Thierry  
; APPLICANT: Haeuw, Jean-Francois  
; APPLICANT: Nguyen Ngoc, Thien  
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant  
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for  
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines  
; Patent No. 6780420  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.  
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/679,750
; FILING DATE: 08-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,500
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-679-750--4

Query Match          54.0%; Score 984; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.4e-90;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYNPYLGFEMGY 69
DB 1 APKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYNPYLGFEMGY 60

QY 70 DWLGRMAYKGSVNGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWRADSKGNYSTGV 129
DB 61 DWLGRMAYKGSVNGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWRADSKGNYSTGV 120

QY 130 SRSEHDTGSPVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYR 188
DB 121 SRSEHDTGSPVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYR 179

RESULT 7
US-09-809-665A-151
; Sequence 151, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-809-665A-151

Query Match          36.8%; Score 671; DB 2; Length 364;
Best Local Similarity 42.4%; Pred. No. 2.6e-58;
Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

QY 1 MKAIFVLNAAPKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTR-----NDQLGAGAFGG 56
DB 11 LSAAVAQAAPQONTFYAGAKAGWASFHDGIEQLDSAKNTDRGTYKGINRNSVTYGVFGG 70

QY 57 YQV--NPYLGF--EMGYDWLGRM-----AYKGSVDNGAFK--AQGVLTAKLGYPIITDDLD 106
DB 71 YQILNQDKLGLAAELGYDFGVRGSEKPKNGKADKKTFRHAAHGATIALKPSYEVLPLDLD 130

QY 107 IYTRLG-GMWRADSKGNVASTGVSRSEHDTGSPVPFAGGVEMAVTRDIATRLLEYQWNN 165
DB 131 VYGVGIALVNNYTYTFNAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLN 188

QY 166 IGDA-----GTGTRPDNGMLSLGVSYRFGQEDAAFPVAPAPAPAPAPAPAPAPAPAP 217
DB 189 AGKASYSTLNRMGATDYSRDISVVSAGLSYRFGQ-GAVPVAAPA-----VETKNFAFS 241

QY 218 DVLFNFKATLKPEGQOQALDQLYTLQSLNMDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQ 277
DB 242 DVLFAGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKESNLKLSORRAE 301

QY 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVGKYE 337
DB 302 TVANYIVSKGAPAAVNTAVGYGEANPVTGATCDKVKGRKALIACLAPDRRVEIEVGKYE 361

QY 338 V 338
DB 362 V 362

RESULT 8
US-09-418-980-8
; Sequence 8, Application US/09418980
; Patent No. 6713071
; GENERAL INFORMATION:
; APPLICANT: Campos, Manuel
; APPLICANT: Baarich, Mary Jo
; APPLICANT: Rosey, Everett
; APPLICANT: Ankendauer, Robert
; APPLICANT: Warren-Stewart, Lynn
; APPLICANT: Suiter, Brian
; APPLICANT: Keach, Robin
; TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
; FILE REFERENCE: PC9854A
; CURRENT APPLICATION NUMBER: US/09/418,980
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-418-980-8

Query Match          36.6%; Score 667; DB 2; Length 364;
Best Local Similarity 42.1%; Pred. No. 6.5e-58;
Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

QY 1 MKAIFVLNAAPKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTR-----NDQLGAGAFGG 56
DB 11 LSAAVAQAAPQONTFYAGAKAGWASFHDGIEQLDSAKNTDRGTYKGINRNSVTYGVFGG 70

QY 57 YQV--NPYLGF--EMGYDWLGRM-----AYKGSVDNGAFK--AQGVLTAKLGYPIITDDLD 106
DB 71 YQILNQDKLGLAAELGYDFGVRGSEKPKNGKADKKTFRHAAHGATIALKPSYEVLPLDLD 130

QY 107 IYTRLG-GMWRADSKGNVASTGVSRSEHDTGSPVPFAGGVEMAVTRDIATRLLEYQWNN 165
DB 131 VYGVGIALVNNYTYTFNAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLN 188

QY 166 IGDA-----GTGTRPDNGMLSLGVSYRFGQEDAAFPVAPAPAPAPAPAPAPAPAPAP 217
DB 189 AGKASYSTLNRMGATDYSRDISVVSAGLSYRFGQ-GAVPVAAPA-----VETKNFAFS 241

QY 218 DVLFNFKATLKPEGQOQALDQLYTLQSLNMDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQ 277
DB 242 DVLFAGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKESNLKLSORRAE 301

QY 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVGKYE 337
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Db 302 TVANYIVSKGAPAAVTVAVGGEANPVGTGCDKVKGRKALIACLAPDRREVEVQVGTKE 361  
Qy 338 V 338  
Db 362 V 362

RESULT 9  
US-09-506-078-45  
; Sequence 45, Application US/09506078  
; Patent No. 6911206  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Products Inc  
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A  
; FILE REFERENCE: DUAL IMMUNE RESPONSE  
; CURRENT APPLICATION NUMBER: US/09/506,078  
; CURRENT FILING DATE: 2000-02-16  
; EARLIER APPLICATION NUMBER: N/A  
; EARLIER FILING DATE: 1999-02-17  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Actinobacillus pleuropneumoniae  
US-09-506-078-45

Query Match 36.6%; Score 667; DB 2; Length 364;  
Best Local Similarity 42.1%; Pred. No. 6.5e-58;  
Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIFVLNAPKDNWTYAGGKLGWSQYHDTGFGYNGFQNNNGPTR----NDQLGAGARFG 56  
Db 11 LSAAVAQAAPQNTFFYAGAKAGWASPHDGIQLDSAKNTDRGTGKYGINRNSVTVYGVFG 70  
Qy 57 YQV---NPYLGF---EMGYDWLGRM---AYKGSVDNGAFK---AQGVQLTAKLGYPTDLDL 106  
Db 71 YQILNQDKLGLAAELGYDYFGRVRSKPKNGKADKTFRHAAGATIALKPSYEVLPDL 130  
Qy 107 IYTRLG-GMWVRADSKGNVASTGVSRSEHDTGVSVPFAGVGEVAVTRDIATRLLEYQWNN 165  
Db 131 VYGVGIALVNTYTKTFNAAQEKVKTRRFOS--SLILGAGVEYAILPELAARVEYQWLNN 188  
Qy 166 IGDA-----GTVGTTRPDNGMLSLGVSYRFGQEDAAPVVPAPAPAPAEVATKHTLKS 217  
Db 189 AGKASYSTLNRMGATDYRSIDSSVAGLSYRFGQ-GAVPVAAPA-----VETKNFASF 241  
Qy 218 DVLNFKATLKPEGQOALDQLYTQLSNMDDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQ 277  
Db 242 DVLFAFGKSNLKPAAATLADAMQTEINNAGLSNAAIQVNGYTDRIIGKEASNLKLSORAE 301  
Qy 278 SVVDYLVAKGIIPAGKISARGNGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337  
Db 302 TVANYIVSKGAPAAVTVAVGGEANPVGTGCDKVKGRKALIACLAPDRRVEVQVGTKE 361  
Qy 338 V 338  
Db 362 V 362

RESULT 10  
US-08-457-997B-2  
; Sequence 2, Application US/08457997B  
; Patent No. 5766608  
; GENERAL INFORMATION:  
; APPLICANT: Kolattukudy, P. E.  
; TITLE OF INVENTION: Otitis Media Vaccine  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calfee, Halter and Griswold  
; STREET: Suite 1800 800 Superior Avenue

CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2688  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,997B  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Golrick, Mary E.  
REGISTRATION NUMBER: 34,829  
REFERENCE/DOCKET NUMBER: 22727/00102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8458  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-457-997B-2

Query Match 36.3%; Score 662.5; DB 1; Length 359;  
Best Local Similarity 43.3%; Pred. No. 1.8e-57;  
Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;

Qy 1 MKAIFVLNAPKDNWTYAGGKLGWSQYHDTGFGYNGFQNNNGPTRNDQLGAGARFG 56  
Db 13 LSAAVAQAAPQNTFFYAGKAGQGSFHDGINNNGAIKKGLSSNTGYRNTTFTYGVFG 72  
Qy 57 YQV---NPYLGFEMGYDWLGRMAYKGSVDNGAFKQ---GVQLTAKLGYPTDLDLIY 108  
Db 73 YQILNQDNFGLAAELGYDDFGRAKLR---EAGPKAKHTNHGAYLSLKGSYEVLGDLVY 129  
Qy 109 IRLGGMWRADSKGNVASTGV---SRSEHDTGVSVPFAGVGEVAVTRDIATRLLEYQWNN 165  
Db 130 GKAGVALVRSYDKFYEDANGTRDHKKGRHTARASGLFAVGAEYAVLPELAVRLEYQWLTR 189  
Qy 166 IG-----DAGTVGTTRPDNGMLSLGVSYRFGQEDAAPVVPAPAPAEVATKHTLKS 218  
Db 190 VYKVRPQDKPNTAINYNPWIGCINAGISYRFGQ---APVVA-----APENVSKTFLNSD 243  
Qy 219 VLFNFKATLKPEGQOALDQLYTQLSNMDDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQ 278  
Db 244 VTFAGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGYTNRIGSDAFNVKLSQERADS 301  
Qy 279 VVDYLVAKGIIPAGKISARGNGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYK 336  
Db 302 VANYFVAKGAAADAISATGYGEANPVGTGCDQVKGKRALIACLPDRRVEIANGTK 359

RESULT 11  
US-08-467-722A-2  
; Sequence 2, Application US/08467722A  
; Patent No. 6030626  
; GENERAL INFORMATION:  
; APPLICANT: Kolattukudy, P. E.  
; TITLE OF INVENTION: Otitis Media Vaccine  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calfee, Halter and Griswold  
; STREET: Suite 1800 800 Superior Avenue  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: U.S.A.  
; ZIP: 44114-2688  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,722A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Golrick, Mary E.  
REGISTRATION NUMBER: 34,899  
REFERENCE/DOCKET NUMBER: 22727/00102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8458  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-722A-2

Query Match 36.3%; Score 662.5; DB 2; Length 359;  
Best Local Similarity 43.3%; Pred. No. 1.8e-57;  
Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;  
QY 1 MKAIFVLNAAPKONTWYAGKLGWSQYHD-----TGFYNGFQNNNGPTRNDQLGAGAFGG 56  
DB 13 LAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSNTGYRRNTFTYGVFG 72  
QY 57 YQV-----NPVLGFEMGYDMLGRMAYKGSVDNGAFKAQ-----GVQLTAKLGYPITDLDIY 108  
DB 73 YQILNQDNFGLAELGYDDFGRKLR---EAGKPKAKHTNHGAYLSLKGSEYELDGLDVY 129  
QY 109 TRLGGMWRADSKGNVASTGV---SRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNN 165  
DB 130 GKAGVALVRSDFYEDANGTRDHKKGRHTARASGLFAVGAAYVLPALAVRLEYQWLTR 189  
QY 166 IG-----DAGTVGTRPDNGMLSLGVSYPFGQEDAAPVVPAPAPAPAPAVATKHTLKSD 218  
DB 190 VGKYPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APEMVSKTFSLSND 243  
QY 219 VLFNFNKATLKPEGQQAOLDQLYTQLSNMDPKDGSVVLGYTRIGSEAYNQQLSEKRAQS 278  
DB 244 VTFAFGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGVTNRIGSDAFNVKLSQERADS 301  
QY 279 VVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGK 336  
DB 302 VANYFVAKGVAADAISATGYGEANPVTGATCDQVKGKRALIACIAPDRRVEIAVNGTK 359

RESULT 12  
US-09-451-184-2  
Sequence 2, Application US/09451184  
Patent No. 6562349  
GENERAL INFORMATION:  
APPLICANT: Kolattukudy, P. E.  
TITLE OF INVENTION: Otitis Media Vaccine  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter and Griswold  
STREET: 1400 McDonald Investment Center,  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2688  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/451,184  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Docherty, Pamela A.  
REGISTRATION NUMBER: 40,591  
REFERENCE/DOCKET NUMBER: 24547/04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8416  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-451-184-2

Query Match 36.3%; Score 662.5; DB 2; Length 359;  
Best Local Similarity 43.3%; Pred. No. 1.8e-57;  
Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;  
QY 1 MKAIFVLNAAPKONTWYAGKLGWSQYHD-----TGFYNGFQNNNGPTRNDQLGAGAFGG 56  
DB 13 LAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSNTGYRRNTFTYGVFG 72  
QY 57 YQV-----NPVLGFEMGYDMLGRMAYKGSVDNGAFKAQ-----GVQLTAKLGYPITDLDIY 108  
DB 73 YQILNQDNFGLAELGYDDFGRKLR---EAGKPKAKHTNHGAYLSLKGSEYELDGLDVY 129  
QY 109 TRLGGMWRADSKGNVASTGV---SRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNN 165  
DB 130 GKAGVALVRSDFYEDANGTRDHKKGRHTARASGLFAVGAAYVLPALAVRLEYQWLTR 189  
QY 166 IG-----DAGTVGTRPDNGMLSLGVSYPFGQEDAAPVVPAPAPAPAPAVATKHTLKSD 218  
DB 190 VGKYPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APEMVSKTFSLSND 243  
QY 219 VLFNFNKATLKPEGQQAOLDQLYTQLSNMDPKDGSVVLGYTRIGSEAYNQQLSEKRAQS 278  
DB 244 VTFAFGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGVTNRIGSDAFNVKLSQERADS 301  
QY 279 VVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGK 336  
DB 302 VANYFVAKGVAADAISATGYGEANPVTGATCDQVKGKRALIACIAPDRRVEIAVNGTK 359

RESULT 13  
US-09-809-665A-153  
Sequence 153, Application US/09809665A  
Patent No. 6790950  
GENERAL INFORMATION:  
APPLICANT: Lowery E., David, et al.  
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions  
FILE REFERENCE: 28341/00435  
CURRENT APPLICATION NUMBER: US/09/809,665A  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: 60/153,453  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: 60/128,689  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 09/545,199  
PRIOR FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 153  
LENGTH: 369  
TYPE: PRT  
ORGANISM: Actinobacillus pleuropneumoniae  
US-09-809-665A-153  
Query Match 35.5%; Score 646.5; DB 2; Length 369;



```
Best Local Similarity 41.1%; Pred. No. 7.4e-56;
Matches 153; Conservative 60; Mismatches 110; Indels 49; Gaps 12;

Qy 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHDTGFYQ-NGFONNNGPTRNDQ-----L 49
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LSAAAVAQAAPQONTFYAGAKVGSSFH----HGVNQLKSGHDDRYNDKTRKYGINRSV 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 50 GAGAFGGYQV----NPYLGEMGYDMLGRMAYKGSVDNGAFK-----AOGVOLTAKLGYP 100
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 TYGVFGGYQILNQNNFGLAELGYDYGRV--RGNVDE--FRTVKHSAHGLNLALKPSYE 122
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 101 ITDLDLYTRLGGWVRADSKGNVASTGVSRSE---HDTGVSPVFAGGVWAVTRDIATRL 158
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 VLPDLGVYGVKGVAVVRNDYK-KYGAENTNESTTKFKLKAATILGAGVEYAILPELAAR 181
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
158 LEYQWVNNIGDAGTV-----GTR-----PONGMLSLGVSRYRFGQEDAAAPVAPAPAPAP 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 VEYQYLNKAGNLKALVRSQTQDVFQYAPDIHSVTAGLSYRFGQGVAVPV-----EPE 235
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 207 EVATKHTFLKSDVLFNFKNATLKPFGQOALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEA 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 EVVTKNFAFSSDVLDFGKSSLPAAATALDAANTEIANGLATPAIQVNGYTDRIGKEA 295
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 267 YNQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 SNLKSQRRAETVANYLVSKGQNPANVTAVGYGEANPVTGATCDVKGKRALIACLAAPDR 355
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 327 RVEIEVKGYKEV 338
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 RVEVQVQGAQNV 367
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-418-980-10
; Sequence 10, Application US/09418980
; Patent No. 6713071
; GENERAL INFORMATION:
; APPLICANT: Campos, Manuel
; APPLICANT: Baarsch, Mary Jo
; APPLICANT: Rosey, Everett
; APPLICANT: Ankenbauer, Robert
; APPLICANT: Warren-Stewart, Lynn
; APPLICANT: Suiter, Brian
; APPLICANT: Keach, Robin
; TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
; FILE REFERENCE: PC9854A
; CURRENT APPLICATION NUMBER: US/09/418,980
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-418-980-10

Query Match 35.1%; Score 639.5; DB 2; Length 369;
Best Local Similarity 40.7%; Pred. No. 3.7e-55;
Matches 151; Conservative 60; Mismatches 113; Indels 47; Gaps 11;

Qy 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHDTGFYQ-NGFONNNGPTRNDQ-----L 49
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LSAAAVAQAAPQONTFYAGAKVGSSFH----HGVNQLKSGHDDRYNDKTRKYGINRSV 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 50 GAGAFGGYQV----NPYLGEMGYDMLGRMAYKGSVDNGAFK-----AOGVOLTAKLGYP 100
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 TYGVFGGYQILNQNNFGLAELGYDYGRV--RGNVDE--FRTVKHSAHGLNLALKPSYE 122
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 101 ITDLDLYTRLGGWVRADSKGNVASTGVSRSE---HDTGVSPVFAGGVWAVTRDIATRL 158
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 VLPDLGVYGVKGVAVVRNDYK-KYGAENTNESTTKFKLKAATILGAGVEYAILPELAAR 182
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
159 EYQWVNNIGDAGTV-----GTR-----PONGMLSLGVSRYRFGQEDAAAPVAPAPAPAP 207
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Query Match 35.1%; Score 639.5; DB 2; Length 369;
Best Local Similarity 40.7%; Pred. No. 3.7e-55;
Matches 151; Conservative 60; Mismatches 113; Indels 47; Gaps 11;

Qy 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHDTGFYQ-NGFONNNGPTRNDQ-----L 49
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LSAAAVAQAAPQONTFYAGAKVGSSFH----HGVNQLKSGHDDRYNDKTRKYGINRSV 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 50 GAGAFGGYQV----NPYLGEMGYDMLGRMAYKGSVDNGAFK-----AOGVOLTAKLGYP 100
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 TYGVFGGYQILNQNNFGLAELGYDYGRV--RGNVDE--FRTVKHSAHGLNLALKPSYE 122
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 101 ITDLDLYTRLGGWVRADSKGNVASTGVSRSE---HDTGVSPVFAGGVWAVTRDIATRL 158
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 VLPDLGVYGVKGVAVVRNDYK-KYGAENTNESTTKFKLKAATILGAGVEYAILPELAAR 182
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
159 EYQWVNNIGDAGTV-----GTR-----PONGMLSLGVSRYRFGQEDAAAPVAPAPAPAP 207
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: November 26, 2005, 00:20:50
Job time : 48 secs
```

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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uspto)

This ...

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 23:51:17 ; Search time 230 Seconds  
(without alignments)  
1055.225 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVLNAPKDNWTYAGG.....DRRVEIVKGYKEVVTQAP 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1813	99.5	344	1 OMPA_KLEPN	P24017 klebsiella
2	1542	84.6	350	1 OMPA_ENTAE	P09146 enterobacte
3	1525.5	83.7	351	1 OMPA_SHIDY	P02935 shigella dy
4	1513.5	83.0	347	2 Q52JK5_ENTSA	Q52JK5 enterobacte
5	1511	82.9	346	1 OMPA_ECO57	P0A910 escherichia
6	1511	82.9	346	1 OMPA_ECOLI	P0A910 escherichia
7	1511	82.9	346	2 Q6W821_SHISO	Q6W821 shigella so
8	1507	82.7	346	2 Q6PNM6_SHIBO	Q6PNM6 shigella bo
9	1505	82.6	346	2 Q9L6J0_ECOLI	Q9L6J0 escherichia
10	1501	82.3	350	2 Q57OT3_SALCH	Q57OT3 salmonella
11	1500	82.3	350	2 Q5PGD5_SALPA	Q5PGD5 salmonella
12	1499	82.2	350	1 OMPA_SALTI	Q8Z780 salmonella
13	1495	82.0	350	1 OMPA_SALTY	P02936 salmonella
14	1487	81.6	379	2 Q8CW76_ECOL6	Q8CW76 escherichia
15	1473	80.8	348	2 Q83RX2_SHIFL	Q83RX2 shigella fl
16	1466	80.4	327	2 Q7X017_SHIFL	Q7X017 shigella fl
17	1381.5	75.8	359	1 OMPA_SERMA	P04845 serratia ma
18	1364	74.8	319	2 Q6QT47_SALGL	Q6QT47 salmonella
19	1325.5	72.7	353	1 OMPA_YERPE	Q8ZG77 yersinia pe
20	1325.5	72.7	353	1 OMPA_YERPS	P38399 yersinia ps
21	1306	71.6	366	2 Q6D6D4_ERWCT	Q6D6D4 erwinia car
22	1289	70.7	368	2 Q7N602_PHOLL	Q7N602 photorhabdu
23	1262.5	69.3	367	2 Q9RM69_ERWCA	Q9RM69 erwinia car
24	1128.5	61.9	238	1 Q9N114_ESCVU	Q9N114 escherichia
25	1112.5	61.0	244	2 Q47880_ESCVU	Q47880 escherichia
26	1111	60.9	243	1 OMPA_BSCFE	P24747 escherichia
27	1110.5	60.9	244	2 Q9N115_ESCVU	Q9N115 escherichia
28	1106	60.7	243	1 OMPA_ESCHE	P24754 escherichia
29	1095.5	60.1	238	2 Q9N123_ENTAE	Q9N123 enterobacte
30	1089	59.7	241	1 OMPA_ESCBL	Q9N124 escherichia
31	1056.5	58.0	238	1 OMPA_CITFR	P24016 citrobacter

#### RESULT 1

ID	OMPA_KLEPN	STANDARD;	PRT;	344 AA.
AC	P24017; O69435;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Outer membrane protein A precursor (Outer membrane protein II).			
GN	Name=ompA;			
OS	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Klebsiella.			
OX	NCBI_TaxID=573;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=RV 308;			
RX	MEDLINE=98192544; PubMed=9524233; DOI=10.1016/S0378-1119(98)00060-2;			
RA	Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,			
RA	Baumann T., Haeuw J.P., Uhlen H., Binz H., Stahl S.;			
RT	"Chromosome sequencing using a PCR-based biotin-capture method			
RT	allowed isolation of the complete gene for the outer membrane protein			
RT	A of Klebsiella pneumoniae."			
RL	Gene 210:93-101(1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE OF 93-335.			
RC	STRAIN=LD1119;			
RX	MEDLINE=92065252; PubMed=1955870;			
RA	Lawrence J.G., Ochman H., Hartl D.L.;			
RT	"Molecular and evolutionary relationships among enteric bacteria."			
RL	J. Gen. Microbiol. 137:1911-1921(1991).			
CC	- FUNCTION: Required for the action of colicins K and L and for the			
CC	stabilization of mating aggregates in conjugation. Serves as a			
CC	receptor for a number of f-even like phages. Also acts as a porin			
CC	with low permeability that allows slow penetration of small			
CC	solute (by similarity).			
CC	- SUBUNIT: Monomer (Probable).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.			
CC	- SIMILARITY: Belongs to the ompA family.			
CC	- SIMILARITY: Contains 1 OmpA-like domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	EMBL; AJ000998; CAA04450.1; -; Genomic DNA.			
DR	EMBL; M63355; AAA25119.1; -; Genomic DNA.			
DR	HSSP; P02934; 1QJP.			
DR	SMR; P24017; 10-195.			
DR	InterPro; IPR006664; Bac.OmpA.			
DR	InterPro; IPR002368; OmpA.			
DR	InterPro; IPR006665; OmpA/MotB.			
DR	InterPro; IPR006690; OMPA_LIKE.			

Q5etv7 enterobacte  
Q9l6i9 salmonella  
Q5etv5 salmonella  
Q9l6i8 shigella fl  
Q5etv9 citrobacter  
P24755 serratia od  
Q5etv8 serratia od  
Q5etv6 serratia sp  
Q6waf8 klebsiella  
Q6waf6 klebsiella  
Q6waf7 klebsiella  
Q6waf9 klebsiella  
Q6wago klebsiella  
Q6wagi klebsiella

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DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMEMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA_1; 1.
DR PROSITE; PS11123; OmpA_2; 1.
KW Conjugation; Ion transport; Membrane; Outer membrane;
KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.
FT SIGNAL 1 ? Potential.
FT CHAIN ? 344 Outer membrane protein A.
FT TRANSMEM 15 28 Potential.
FT TRANSMEM 48 60 Potential.
FT TRANSMEM 63 78 Potential.
FT TRANSMEM 90 100 Potential.
FT TRANSMEM 104 119 Potential.
FT TRANSMEM 140 151 Potential.
FT TRANSMEM 157 173 Potential.
FT TRANSMEM 179 190 Potential.
FT REPEAT 199 200 1.
FT REPEAT 201 202 2.
FT REPEAT 203 204 3.
FT REPEAT 205 206 4.
FT DOMAIN 208 336 OmpA-like.
FT REGION 199 206 4 X 2 AA tandem repeats of A-P.
FT DISULFID 309 321 By similarity.
FT CONFLICT 335 335 Y -> I (in Ref. 2).
SQ SEQUENCE 344 AA; 37061 MW; AC8AAAE3B7871B16 CRC64;

Query Match 99.5%; Score 1813; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-131;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAIFVLNAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQVN 60
Db 1 MKAIFVLNAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQVN 60
Qy 61 PYLGFENGWDLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDIYTRLGGWVRADS 120
Db 61 PYLGFENGWDLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDIYTRLGGWVRADS 120
Qy 121 KGNVASTGVSRSHTDGTGSPVFAGGVWAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGM 180
Db 121 KGNVASTGVSRSHTDGTGSPVFAGGVWAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGM 180
Qy 181 LSLGVSYRFQGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
Db 181 LSLGVSYRFQGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
Qy 241 TQLSNMDPKDGSVAVLYGTDRIQSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
Db 241 TQLSNMDPKDGSVAVLYGTDRIQSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEVKGKEVVTOP 342
Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEVKGKEVVTOP 342

RESULT 2
OMPA_ENTAE STANDARD; PRT; 350 AA.
AC P09146;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Outer membrane protein A precursor.
GN Name=ompA;
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]

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RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE-84108348; PubMed-6363059;
RA Braun G., Cole S.T.;
RT "Molecular characterization of the gene coding for major outer
RT membrane protein OmpA from Enterobacter aerogenes.";
RL Eur. J. Biochem. 137:495-500(1983).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the ompA family.
CC -!- SIMILARITY: Contains 1 OmpA-like domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X00254; CAA25062.1; -; Genomic_DNA.
DR PIR; S07222; S07222.
DR HSSP; P02934; 1QJP.
DR SMR; P09146; 22-201.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA LIKE.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMEMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA_1; 1.
DR PROSITE; PS11123; OmpA_2; 1.
KW Conjugation; Ion transport; Membrane; Outer membrane;
KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.
FT SIGNAL 1 21
FT CHAIN 22 350 Outer membrane protein A.
FT TRANSMEM 27 40 Potential.
FT TRANSMEM 59 71 Potential.
FT TRANSMEM 74 89 Potential.
FT TRANSMEM 101 111 Potential.
FT TRANSMEM 115 130 Potential.
FT TRANSMEM 146 157 Potential.
FT TRANSMEM 163 179 Potential.
FT TRANSMEM 185 196 Potential.
FT REPEAT 205 206 1.
FT REPEAT 207 208 2.
FT REPEAT 209 210 3.
FT REPEAT 211 212 4.
FT DOMAIN 214 342 OmpA-like.
FT REGION 205 212 4 X 2 AA tandem repeats of A-P.
FT DISULFID 315 327 By similarity.
SQ SEQUENCE 350 AA; 37575 MW; 6276C6F2F21065DA CRC64;

Query Match 84.6%; Score 1542; DB 1; Length 350;
Best Local Similarity 87.5%; Pred. No. 5e-110;
Matches 295; Conservative 10; Mismatches 26; Indels 6; Gaps 2;

Qy 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
Db 18 VAQAAPKONTWYAGKLGWSQYHDTGFWY-NSNLNNGPTHESQLGAGAFGGYQVNPYLGF 76
Qy 66 ENGVDWLGSMAYKGSVDNGAFKAQGVLTAKLGYPTDLDIYTRLGGWVRADSKNYA 125
Db 77 EMGYDWLGMPYKGVKVGAFSSQAVQLTAKLGYPTDLDIYTRLGGWVRADSKNYA 131
Qy 126 STGVSRSRSHDGTGSPVFAGGVWAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGV 185

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Db 132 SNSIAGNDHDTGSPVPAGGVEHWMTRDIATRLLEYQWNNIGDAGTVGVPRDNGMLSVGV 191
Qy 186 SYRFGQSDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 192 SYRFGQSDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 251
Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGHGESNPVT 305
Db 252 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGHGESNPVT 311
Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOP 342
Db 312 GNTCDNVKARAALIDCLAPDRRVAIEVKYKDVVTOP 348

RESULT 3
Query Match 83.7%; Score 1525.5; DB 1; Length 351;
Best Local Similarity 84.6%; Pred. No. 9.3e-109;
Matches 285; Conservative 20; Mismatches 27; Indels 5; Gaps 1;
AC P02935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II).
GN Name=ompA;
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA MEDLINE=82221414; PubMed=6283478;
RX Braun G., Cole S.T.;
RT "The nucleotide sequence coding for major outer membrane protein OmpA
of Shigella dysenteriae.";
RL Nucleic Acids Res. 10:2367-2378 (1982).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the ompA family.
CC -!- SIMILARITY: Contains 1 OmpA-like domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ENBL; V01344; CAA24638.1; -; Genomic_DNA.
DR PIR; A03435; MMEBAD.
DR HSSP; P02935; 1QJP.
DR SMR; P02935; 22-202.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA LIKE.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
DR PROSITE; PS1123; OmpA; 2; 1.
DR Conjugation; Ion transport; Membrane; Outer membrane;
KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.
FT SIGNAL 1 21
FT CHAIN 22 351 Outer membrane protein A.
FT TRANSMEM 27 40 Potential.
FT TRANSMEM 55 67 Potential.
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FT TRANSMEM 70 85 Potential.
FT TRANSMEM 97 107 Potential.
FT TRANSMEM 111 126 Potential.
FT TRANSMEM 147 158 Potential.
FT TRANSMEM 164 180 Potential.
FT TRANSMEM 186 197 Potential.
FT REPEAT 206 207 1.
FT REPEAT 208 209 2.
FT REPEAT 210 211 3.
FT REPEAT 212 213 4.
FT DOMAIN 215 343 OmpA-like.
FT REGION 206 213 4 X 2 AA tandem repeats of A-P.
FT DISULFID 316 328 By similarity.
SQ SEQUENCE 351 AA; 37741 MW; 1499AA5F5395B35B CRC64;

Query Match 83.7%; Score 1525.5; DB 1; Length 351;
Best Local Similarity 84.6%; Pred. No. 9.3e-109;
Matches 285; Conservative 20; Mismatches 27; Indels 5; Gaps 1;
Qy 6 VLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAGGYQVNPYLGF 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----DNNGPTHEHQLGAGAGGYQVNPVGF 72
Qy 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADSKGNYA 125
Db 73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADTKAHNN 132
Qy 126 STGVSRSSEHDTGSPVFAGGVWAVTRDIATRLLEYQWNNIGDAGTVGVPRDNGMLSLGV 185
Db 133 VTGSEKNHDTGSPVFAGGVWAVTRDIATRLLEYQWNNIGDAGTVGVPRDNGMLSLGV 192
Qy 186 SYRFGQSDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 193 SYRFGQSDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 252
Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGHGESNPVT 305
Db 253 LDPKDGSAVVLGYTDRIGSDAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGHGESNPVT 312
Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOP 342
Db 313 GNTCDNVKARAALIDCLAPDRRVEIEVKYKDVVTOP 349

RESULT 4
Q52JK5_ENTSA PRELIMINARY; PRT; 347 AA.
ID Q52JK5_ENTSA PRELIMINARY; PRT; 347 AA.
AC Q52JK5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OmpA.
GN Name=ompA;
OS Enterobacter sakazakii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=28141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 51329;
RA Mohan Nair M.K., Venkitanarayanan K.S.;
RT "Cloning and Sequencing of the Major Outer Membrane Protein Gene ompA
and Development of A Specific PCR for Rapid Detection of Enterobacter
RT sakazakii in Infant Formula.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ000206; AAY18798.1; -; Genomic DNA.
SQ SEQUENCE 347 AA; 37054 MW; 84D85148F54260C2 CRC64;

Query Match 83.0%; Score 1513.5; DB 2; Length 347;
Best Local Similarity 84.9%; Pred. No. 7.7e-108;
Matches 287; Conservative 16; Mismatches 24; Indels 11; Gaps 3;
Qy 6 VLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAGGYQVNPYLGF 65
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Db 248 LDPKDGSVVGLYDTRIGSDAYNQGLSERRAQSVVDYLSKGPADKISARGMESNPVT 307  
Qy 306 GNTCDNVKARAALIDCLAPRRVEIEVKGVEVVTQP 342  
Db 308 GNTCDNVKQARAALIDCLAPRRVEIEVKGIDVVTQP 344

RESULT 6  
OMP\_A\_ECOLI  
ID OMP\_A\_ECOLI STANDARD; PRT; 346 AA.  
AC POA9IO; P02934;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Outer membrane protein A precursor (Outer membrane protein II\*)  
OS Name=ompA; Synonyms=con, tolG, tut; OrderedLocusName=b0957;  
OC Escherichia coli  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=K12;  
RX MEDLINE=81053729; PubMed=6253901;  
RA Beck E., Bremer E.;  
RT "Nucleotide sequence of the gene ompA coding the outer membrane  
protein II of Escherichia coli K-12";  
RL Nucleic Acids Res. 8:3011-3024(1980).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=K12;  
RX MEDLINE=81170587; PubMed=6260961;  
RA Movva N.R., Nakamura K., Inouye M.;  
RT "Gene structure of the OmpA protein, a major surface protein of  
Escherichia coli required for cell-cell interaction";  
RL J. Mol. Biol. 143:317-328(1980).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Ohnina T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,  
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
Yano M., Horiuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 12.7-28.0 min region on the linkage map";  
RL DNA Res. 3:137-155(1996).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=K12 / MGL165;  
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474(1997).  
RN [5]  
RP PROTEIN SEQUENCE OF 22-346.  
RC STRAIN=K12;  
RX MEDLINE=81054820; PubMed=7001461;  
RA Chen R., Schmidmayr W., Kramer C., Chen-Schmeisser U., Henning U.;  
RT "Primary structure of major outer membrane protein II (ompA protein)-  
of Escherichia coli K-12";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596(1980).  
RN [6]  
RP PROTEIN SEQUENCE OF 22-34.  
RC STRAIN=K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;

RT "Comparing the predicted and observed properties of proteins encoded  
in the genome of Escherichia coli K-12";  
RL Electrophoresis 18:1259-1313(1997).  
RN [7]  
RP PROTEIN SEQUENCE OF 22-32.  
RC STRAIN=K12 / W3110;  
RA Pasquall C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J.,  
Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,  
Hochstrasser D.F.;  
RL Submitted (SEP-1994) to Swiss-Prot.  
RN [8]  
RP PROTEIN SEQUENCE OF 22-26.  
RC STRAIN=K12 / W3110;  
RX MEDLINE=98291876; PubMed=9629924;  
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,  
Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;  
RT "Extraction of membrane proteins by differential solubilization for  
separation using two-dimensional gel electrophoresis";  
RL Electrophoresis 19:837-844(1998).  
RN [9]  
RP MUTANTS RESISTANT TO PHAGE ENTRY.  
RX MEDLINE=84264337; PubMed=6086577;  
RA Morona R., Klose M., Henning U.;  
RT "Escherichia coli K-12 outer membrane protein (OmpA) as a  
bacteriophage receptor: analysis of mutant genes expressing altered  
proteins";  
RL J. Bacteriol. 159:570-578(1984).  
RN [10]  
RP MUTANTS RESISTANT TO PHAGE ENTRY.  
RX MEDLINE=86033606; PubMed=3902787;  
RA Morona R., Kramer C., Henning U.;  
RT "Bacteriophage receptor area of outer membrane protein OmpA of  
Escherichia coli K-12";  
RL J. Bacteriol. 164:539-543(1985).  
RN [11]  
RP PORIN ACTIVITY.  
RC STRAIN=K12;  
RX MEDLINE=92129334; PubMed=1370823;  
RA Sugawara E., Nikaido H.;  
RT "Pore-forming activity of OmpA protein of Escherichia coli";  
RL J. Biol. Chem. 267:2507-2511(1992).  
RN [12]  
RP SUBCELLULAR LOCATION.  
RX PubMed=7813480;  
RA Kuhn A., Kiefer D., Koehne C., Zhu H.-Y., Tschantz W.R., Dalbey R.E.;  
RT "Evidence for a loop-like insertion mechanism of pro-Omp A into the  
inner membrane of Escherichia coli";  
RL Eur. J. Biochem. 226:891-897(1994).  
RN [13]  
RP TOPOLOGY.  
RX MEDLINE=94148615; PubMed=8106193;  
RA Gromiha M.M., Ponnuswamy P.K.;  
RT "Prediction of transmembrane beta-strands from hydrophobic  
characteristics of proteins";  
RL Int. J. Pept. Protein Res. 42:420-431(1993).  
RN [14]  
RP TOPOLOGY.  
RX MEDLINE=99296577; PubMed=10368142;  
RA Koebnik R.;  
RT "Structural and functional roles of the surface-exposed loops of the  
beta-barrel membrane protein OmpA from Escherichia coli";  
RL J. Bacteriol. 181:3688-3694(1999).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.  
RX MEDLINE=99023200; PubMed=9808047;  
RA Pautsch A., Schulz G.E.;  
RT "Structure of the outer membrane protein A transmembrane domain";  
RL Nat. Struct. Biol. 5:1013-1017(1998).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).  
RX MEDLINE=20229895; PubMed=10764596; DOI=10.1006/jmbi.2000.3671;  
RA Pautsch A., Schulz G.E.;  
RT "High-resolution structure of the OmpA membrane domain";

RL J. Mol. Biol. 298:273-282 (2000).  
 RN [17]  
 RP STRUCTURE BY NMR OF 22-197.  
 RX PubMed=11276254; DOI=10.1038/86214;  
 RA Atora A., Abildgaard F., Bushweller J.H., Tamm L.K.;  
 RT "Structure of outer membrane protein A transmembrane domain by NMR  
 RT spectroscopy.";  
 RL Nat. Struct. Biol. 8:334-338 (2001).  
 RN [18]  
 RP MASS SPECTROMETRY.  
 RX MEDLINE=20222957; PubMed=10757971; DOI=10.1021/b1000150m;  
 RA le Coutre J., Whiteledge J.P., Gross A., Turk E., Wright E.M.,  
 RA Kaback H.R., Faull K.F.;  
 RT "Proteomics on full-length membrane proteins using mass  
 RT spectrometry.";  
 RL Biochemistry 39:4237-4242 (2000).  
 CC -/- FUNCTION: Required for the action of colicins K and L and for the  
 CC stabilization of mating aggregates in conjugation. Serves as a  
 CC receptor for a number of T-even like phages. Also acts as a porin  
 CC with low permeability that allows slow penetration of small  
 CC solutes.  
 CC -/- SUBUNIT: Monomer (Probable).  
 CC -/- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -/- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346;  
 CC NOTE=Ref.18.  
 CC -/- SIMILARITY: Belongs to the ompA family.  
 CC -/- SIMILARITY: Contains 1 OmpA-like domain.  
 CC -----  
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 CC removed.  
 CC -----  
 CC EMBL; V00307; CAA23588.1; -; Genomic DNA.  
 CC EMBL; D90733; BAA35715.1; -; Genomic DNA.  
 CC EMBL; D90734; BAA35722.1; -; Genomic DNA.  
 CC EMBL; U00096; AAC74043.1; -; Genomic\_DNA.  
 CC F1R; A93707; MRECA.  
 CC PDB; 1BXW; X-ray; A=22-192.  
 CC PDB; 1G90; NMR; A=22-197.  
 CC PDB; 1QJP; X-ray; A=22-192.  
 CC SWISS-2DPAGE; POA910; COLI.  
 CC ECO2DBASE; F024.5; 6TH EDITION.  
 CC ECO2DBASE; F028.0; 6TH EDITION.  
 CC ECO2DBASE; F033.0; 6TH EDITION.  
 CC ECO2DBASE; F033.1; 6TH EDITION.  
 CC EcoGene; EH0663; -.  
 CC EcoGene; EG10669; ompA.  
 CC InterPro; IPR006664; Bac OmpA.  
 CC InterPro; IPR002368; OmpA.  
 CC InterPro; IPR006665; OmpA/MotB.  
 CC InterPro; IPR006690; OMPA LIKE.  
 CC InterPro; IPR000498; OmpA\_tmem.  
 CC Pfam; PF00691; OmpA; 1.  
 CC Pfam; PF01389; OmpA membrane; 1.  
 CC PRINTS; PR01021; OMPADOMAIN.  
 CC PRINTS; PR01022; OUTRMBRANEA.  
 CC ProDom; PD000930; OmpA/MotB; 1.  
 CC PROSITE; PS01068; OMPA\_1; 1.  
 CC PROSITE; PS1123; OMPA\_2; 1.  
 CC 3D-structure; Complete proteome; Conjugation;  
 KW Direct protein sequencing; Ion transport; Membrane; Outer membrane;  
 KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.

Query Match 82.9%; Score 1511; DB 1; Length 346;  
 Best Local Similarity 84.9%; Pred. No. 1-2e-107;  
 Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;  
 QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNQNNPTNDQLGAGAFGGYQVNPYLGF 65  
 Db 18 VAQAAPKONTWYTGAKLGWSQYHDTGFI-----NNGPHTHENQLGAGAFGGYQVNPYVGF 72

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLGGMVWRADSKNYA 125  
 Db 73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPIITDDLDIYTRLGGMVWRADTKSN -- 130  
 QY 126 STGVSRSEHDTGVSFVAGGVWAVTRDIATRLVQVWVNNIGDAGTVGTRPDNGMLSLGV 185  
 Db 131 --VYGNKNDHTGVSFVAGGVVATPEIATRLVQVWVNNIGDAGTVGTRPDNGMLSLGV 187  
 QY 186 SYRFGQEDAAVVPAPAPAPAPAVATKHFTLKSDVLFNFKATLKPESQOALDOLYTOLSN 245  
 Db 188 SYRFGQEAAPVVPAPAPAPAPAVQTKHFTLKSDVLFNFKATLKPESQOALDOLYTOLSN 247  
 QY 246 MPKKGSAVVLGYTDTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVT 305  
 Db 248 LDPKGSVVVLGYTDTRIGSDAYNQOLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVT 307  
 QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTPQ 342  
 Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIGKDVVTPQ 344  
 RESULT 7  
 Q6W821 SHISO  
 ID Q6W821 SHISO PRELIMINARY; PRT; 346 AA.  
 AC Q6W821;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Outer membrane protein A precursor.  
 GN Names=ompA;  
 OS Shigella sonnei.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 OC NCBI\_TaxID=624;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=USMSS2;  
 RA Kirpal-Kaur B., Mohd Zaki S., Asma I., Ravichandran M.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY05874; AAP74759.1; -; Genomic\_DNA.  
 DR SMR; Q6W821; 22-197.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR006664; Bac OmpA.  
 DR InterPro; IPR001035; MotF.  
 DR InterPro; IPR002368; OmpA.  
 DR InterPro; IPR006665; OmpA/MotB.  
 DR InterPro; IPR006690; OMPA LIKE.  
 DR Pfam; PF00691; OmpA; 1.  
 DR Pfam; PF01389; OmpA membrane; 1.  
 DR PRINTS; PR01023; NAFLGMOTY.  
 DR PRINTS; PR01021; OMPADOMAIN.  
 DR PRINTS; PR01022; OUTRMBRANEA.  
 DR ProDom; PD000930; OmpA/MotB; 1.  
 DR PROSITE; PS01068; OMPA; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 346 AA; 37201 MW; 195147734CDF8B04 CRC64;

Query Match 82.9%; Score 1511; DB 2; Length 346;  
 Best Local Similarity 84.9%; Pred. No. 1.2e-107;  
 Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;  
 QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNQNNPTNDQLGAGAFGGYQVNPYLGF 65  
 Db 18 VAQAAPKONTWYTGAKLGWSQYHDTGFI-----NNGPHTHENQLGAGAFGGYQVNPYVGF 72  
 QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLGGMVWRADSKNYA 125  
 Db 73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPIITDDLDIYTRLGGMVWRADTKSN -- 130

D	b		131	--VGKKNHDTGVSVPFAGGVVEYAITPTBIATRLRYEQWVNNIGDAHTI	GTRPDNGMLSLGV	187
Q	y		186	SYRFGQBDAAPVAPAPAPAEVATKHFTLKSDVLFNFNKATLKP	EQGQAALDQLYTQSLN	245
D	b		188	SYRFGQGEAAPVAPAPAPAEVQTGHFTLKSDVLFNFNKATLKP	EGQAALLDLYSOLSN	247
Q	y		246	MDPKDGSAVLGYTDRTGSEAYNQOLSERKAQSVDVYLVAKGIPAKGI	PAGKISAROMGSNPVT	305
D	b		248	LDDPKDGSVVLLGYTDRIGSDAYNOGLSERRAQSVDVYLISKGIPVDKI	SARGMGSSNPVT	307
Q	y		306	GNTCDNVKARAALIDCLADPDRRVIEVKYKEVVTQP	342	
D	b		308	GNTCDNVKQRAALIDCLADPDRRVIEVKGIKDVTQP	344	
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RESULT 9						
Q9L6J0_ECOLI						
ID	Q9L6J0_ECOLI PRELIMINARY;		PRT;	346 AA.		
AC	Q9L6J0;					
DT	01-OCT-2000 (TrEMBLrel. 15, Created)					
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)					
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)					
DE	Outer membrane protein A.					
GN	Name=ompA;					
OS	Escherichia coli.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Escherichia.					
OX	NCBI_TaxID=562;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=RS218;					
RA	Wang Y., Kim K.S.;					
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.					
RM	EMBL; AF2344269; AAC37887.1.; -; Genomic_DNA.					
DR	HSP; P02934; 1QJP.					
DR	SMR; Q9L6J0; 22-197.					
GO	GO: 0016021; C:integral to membrane; IEA.					
DR	GO: GO: 0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.					
DR	GO: GO: 0005198; F:structural molecule activity; IEA.					
DR	InterPro; IPR006664; Bac OmpA.					
DR	InterPro; IPR001035; MotY.					
DR	InterPro; IPR002368; OmpA.					
DR	InterPro; IPR006665; OmpA/MotB.					
DR	InterPro; IPR006690; OMPA LIKE.					
DR	InterPro; IPR000498; OmpA_tmtn.					
DR	Pfam; PF00691; OmpA_1.					
DR	Pfam; PF01389; OmpA_membrane; 1.					
DR	PRINTS; PR01023; NAPFLGMOTY.					
DR	PRINTS; PR01021; OMPADMAMIN.					
DR	PRINTS; PR01022; OUTRRMBRANEA.					
DR	ProDom; PD000930; OmpA/MotB; 1.					
DR	PROSITE; PS01068; OMPA; 1.					
SQ	SEQUENCE 346 AA; 37188 MW; 5736077E41BD84C3 CRC64;					
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Query Match 82.6%; Score 1505; DB 2; Length 346;						
Best Local Similarity 84.3%; Pred. No. 3.4e-107;						
Matches 284; Conservative 18; Mismatches 25; Indels 10; Gaps 2						
Qy	6	VLNAA PKDN TWYAG KG LGSQYHD TGFY GN GFQN NGPTRNDQLG AGAFGGYQVN PYLG F	65			
D	b	18 VAQAAPKDNTWTYTGA KLGW SYHD TGFI-----NNNGPTHENOLGAGA FG YQVN PYVGF	72			
Qy	66	EMG VDW LG RMAY KGS VD NGA FKAG VOL TAKL GP IPTDDLDIYTRLG GMVRADS KN YA	125			
D	b	73 EMG VDW LG R MPY KGS VENG AY KA GV OL TAKL GP IPTDDLVYTRLG GMVRADTK SN--	130			
Qy	126	STGYSRSEHDTGPS VP FAGGVEMA VT RDIA TRLEYQWVN NIC DACTVGTCTR PDNGMLS LCV	185			
D	b	131 --VGKKNHDTGVSVPFAGGVVEYAITPTBIATRLRYEQWVNNIGDAHTI	187			
Qy	186	SYRFGQBDAA PV APAP AE VAT KH FT LKS DV LFNFNK AT L KP EG QA ALD QL YT QS LN	245			
D	b	188 SYRFGQE AAP V PA PA PA PE VO TH FT LKS DV LF NK AT L KP EG QA ALD QL Y SOL SN	247			

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QY 246 MDPKGSVVLGYTDRIGSAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGENPVT 305
Db 248 LDPKGSVVLGYTDRIGSAYNQALSERRAQSVVDYLISKGIPADKISARGMGENPVT 307
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344

RESULT 10
Q57QT3_SALCH
ID Q57QT3_SALCH PRELIMINARY; PRT; 350 AA.
AC Q57QT3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Putative hydrogenase, membrane component.
GN Name=ompA; OrderedLocusNames=SC1022;
OS Salmonella cholerae-suis (Salmonella enterica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
[1]
NCBI_TaxID=591;
RE NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RT Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
DR EMBL; AE017220; AAY64928.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 350 AA; 37491 MW; 7C3529A442E234FC CRC64;

Query Match 82.3%; Score 1501; DB 2; Length 350;
Best Local Similarity 83.1%; Pred. No. 7.1e-107;
Matches 280; Conservative 25; Mismatches 26; Indels 6; Gaps 2;

QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNQNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----NNDGPTHEQLGAGAFGGYQVNPYV 72
QY 66 EMGYDNLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDDLDIYTRLGGMWRADSKGNYA 125
Db 73 EMGYDNLGRMPYKGDNINGAYKAGQVOLTAKLGYPTDDLDVYTRLGGMWRADTKSNVP 132
QY 126 STGVSRSRSHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 133 G-GPSTKDHDTGVSVPFAGGIEVATPEIATRLLEYQWVNNIGDANTIGTRPDNGLLSVG 191
QY 186 SYRFGQEDAAPVVAAPAPAPAPAVATKHTLKSVDLNFENKATLKPEGQALDQLYTQLSN 245
Db 192 SYRFGQEAAPVVAAPAPAPAPAVETQTKHTLKSVDLNFENKSTLKPEGQALDQLYSQLN 251
QY 246 MDPKGSVVLGYTDRIGSAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGENPVT 305
Db 252 LDPKGSVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPADKISARGMGENPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
Db 312 GNTCDNVKPRALIDCLAPDRRVEIEVKGVKDVVTQP 348

RESULT 11
QSPGD5_SALPA
ID QSPGD5_SALPA PRELIMINARY; PRT; 350 AA.
AC QSPGD5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Outer membrane protein A.
DE Outer membrane protein A.
```

```
GN Name=ompA; OrderedLocusNames=SPAL1780;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ngl470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollak S., Sabo A., Meyer R., Bieri T., Ozeraky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Naeh W., Miner T., Minx P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RA "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
DR EMBL; CP000026; AAV77696.1; -; Genomic_DNA.
DR SMR; QSPGD5; 22-201.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR001035; MotY.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA LIKE.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01023; NAFUGMOTY.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMBRANE.
DR PROSITE; PS01068; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Complete proteome.
SQ SEQUENCE 350 AA; 37492 MW; 863F29A442EF8F91 CRC64;

Query Match 82.3%; Score 1500; DB 2; Length 350;
Best Local Similarity 83.1%; Pred. No. 8.5e-107;
Matches 280; Conservative 25; Mismatches 26; Indels 6; Gaps 2;

QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNQNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----NNDGPTHEQLGAGAFGGYQVNPYV 72
QY 66 EMGYDNLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDDLDIYTRLGGMWRADSKGNYA 125
Db 73 EMGYDNLGRMPYKGDNINGAYKAGQVOLTAKLGYPTDDLDVYTRLGGMWRADTKSNVP 132
QY 126 STGVSRSRSHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 133 G-GPSTKDHDTGVSVPFAGGIEVATPEIATRLLEYQWVNNIGDANTIGTRPDNGLLSVG 191
QY 186 SYRFGQEDAAPVVAAPAPAPAPAVATKHTLKSVDLNFENKATLKPEGQALDQLYTQLSN 245
Db 192 SYRFGQEAAPVVAAPAPAPAPAVETQTKHTLKSVDLNFENKSTLKPEGQALDQLYSQLN 251
QY 246 MDPKGSVVLGYTDRIGSAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGENPVT 305
Db 252 LDPKGSVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPADKISARGMGENPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
Db 312 GNTCDNVKPRALIDCLAPDRRVEIEVKGVKDVVTQP 348

RESULT 12
OMPA_SALTI
ID OMPA_SALTI STANDARD; PRT; 350 AA.
AC Q827S0; Q7C962;
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DT 13-SEP-2005 (Rel. 48, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Outer membrane protein A precursor.  
 GN Name=ompA; OrderedLocusNames=STY1091, t1850;  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felkwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen R.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=TY2 / ATCC 700931;  
 RX MEDLINE=22531367; PubMed=12644504;  
 RI DOI=10.1128/JB.185.7.2330-2337.2003;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burland V., Kodyanani V., Schwartz B.C., Blattner F.R.;  
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
 RT and CT18.";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 CC -1- FUNCTION: Required for the action of colicins K and L and for the  
 CC stabilization of mating aggregates in conjugation. Serves as a  
 CC receptor for a number of T-even like phages. Also acts as a porin  
 CC with low permeability that allows slow penetration of small  
 CC solutes (By similarity).  
 CC -1- SUBUNIT: Monomer (Probable).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -1- SIMILARITY: Belongs to the ompA family.  
 CC -1- SIMILARITY: Contains 1 OmpA-like domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: AL627269; CAD08196.1; -; Genomic DNA.  
 CC EMBL: AE016840; AA069468.1; -; Genomic DNA.  
 CC HSP: P02934; IQJP.  
 CC SHR: Q82750; 22-201.  
 CC InterPro: IPR006664; Bac\_OmpA.  
 CC InterPro: IPR002368; OmpA.  
 CC InterPro: IPR006665; OmpA/MotB.  
 CC InterPro: IPR006690; OMPA\_LIKE.  
 CC InterPro: IPR000498; OmpA\_tmam.  
 CC Pfam: PF00691; OmpA; 1.  
 CC Pfam: PF01389; OmpA membrane; 1.  
 CC PRINTS: PR01021; OMPADOMAIN.  
 CC PRINTS: PR01022; OUTRMWBRANEA.  
 CC ProDom: PD000930; OmpA/MotB; 1.  
 CC PROSITE: PS01088; OmpA\_1; 1.  
 CC PROSITE: PSS1123; OmpA\_2; 1.  
 CC Complete proteome; Conjugation; Ion transport; Membrane;  
 CC Outer membrane; Phage recognition; Porin; Repeat; Signal;  
 CC Transmembrane; Transport.  
 KW SIGNAL 1 21 By similarity.  
 KW CHAIN 22 350 Outer membrane protein A.  
 FT TRANSMEM 27 40 Potential.  
 FT TRANSMEM 55 67 Potential.

FT TRANSMEM 70 85 Potential.  
 FT TRANSMEM 97 107 Potential.  
 FT TRANSMEM 111 126 Potential.  
 FT TRANSMEM 146 157 Potential.  
 FT TRANSMEM 163 179 Potential.  
 FT TRANSMEM 185 196 Potential.  
 FT REPEAT 205 206 1.  
 FT REPEAT 207 208 2.  
 FT REPEAT 209 210 3.  
 FT REPEAT 211 212 4.  
 FT DOMAIN 214 342 OmpA-like.  
 FT REGION 205 212 4 X 2 AA tandem repeats of A-P.  
 FT DISULFID 315 327 By similarity.  
 SQ SEQUENCE 350 AA; 37477 MW; EB90059DFCADF3 CRC64;  
 Query Match 82.2%; Score 1499; DB 1; Length 350;  
 Best Local Similarity 82.8%; Pred. No. 1e-106;  
 Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;  
 QY 6 VLNAAPKDNWYAGGKLGMSQYHDTGFGYNGFNQNGPTRNDQLGAGAFGQVNPYLG 65  
 DB 18 VAQAAPKDNWYAGAKLGMSQYHDTGFI----HNDGPTHENQLGAGAFGQVNPYVG 72  
 QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLCGMWRADSKGNYA 125  
 DB 73 EMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPTDLDIYTRLCGMWRADTKSNVP 132  
 QY 126 STGVSRSSEHDTGVSVPFAGSVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185  
 DB 133 G-GASTYKDHDTGVSVPFAGIEIYATPEIATRLLEYQWVNNIGDANTIGTRPDNGLLSVG 191  
 QY 186 SYRFGQEDAAPVAP 245  
 DB 192 SYRFGQEDAAPVAP 251  
 QY 246 MPKQGSAAVLGYTDRIQSEAYNQQLSEKRAQSVVDYLVAKGTPAGKISARGGSENPVT 305  
 DB 252 LQPKDGSVVVLGFTDRIGSDAYNQQLSEKRAQSVVDYLVAKGTPAGKISARGGSENPVT 311  
 QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVVTP 342  
 DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVVTP 348

## RESULT 13

OMPA\_SALTY STANDARD; PRT; 350 AA.  
 AC P02936;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Outer membrane protein A precursor (Outer membrane protein 33K) (Outer  
 DE membrane major heat-modifiable protein).  
 GN Name=ompA; OrderedLocusNames=STM1070;  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=83287368; PubMed=6349993;  
 RA Freidl R., Cole S.T.;  
 RT "Cloning and molecular characterization of the ompA gene from  
 RT Salmonella typhimurium.";  
 RL Eur. J. Biochem. 134:497-502(1983).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
 RA McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
RL Ltr2.";  
CC Nature 413:852-856(2001).  
CC -1- FUNCTION: Required for the action of colicins K and L and for the  
CC stabilization of mating aggregates in conjugation. Serves as a  
CC receptor for a number of T-even like phages. Also acts as a porin  
CC with low permeability that allows slow penetration of small  
CC solutes (By similarity).  
CC -1- SUBUNIT: Monomer (Probable).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
CC -1- SIMILARITY: Belongs to the ompA family.  
CC -1- SIMILARITY: Contains 1 OmpA-like domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC ENBL; X02006; CAA26037.1; -; Genomic DNA.  
DR ENBL; AE008746; AAL20003.1; -; Genomic\_DNA.  
DR PIR; A03436; MMEBAT.  
DR HSSP; P02934; 1QJP.  
DR SMR; P02936; 22-201.  
DR StyGene; SG10263; ompA.  
DR InterPro; IPR006664; Bac\_OmpA.  
DR InterPro; IPR002368; OmpA.  
DR InterPro; IPR006665; OmpA/MotB.  
DR InterPro; IPR006690; OMPA LIKE.  
DR InterPro; IPR000498; OmpA\_tmemb.  
DR Pfam; PF00691; OmpA; 1.  
DR Pfam; PF01389; OmpA membrane; 1.  
DR PRINTS; PR01021; OMPADOMAIN.  
DR PRINTS; PR01022; OUTRMMBRANE.  
DR ProDom; PD000930; OmpA/MotB; 1.  
DR ProSite; PS01068; OMPA; 1; 1.  
DR ProSite; PS1123; OMPA; 2; 1.  
KW Complete proteome; Conjugation; Ion transport; Membrane;  
KW Outer membrane; Phage recognition; Porin; Repeat; Signal;  
KW Transmembrane; Transport.  
FT SIGNAL 1 21 By similarity.  
FT CHAIN 22 350 Outer membrane protein A.  
FT TRANSMEM 27 40 Potential.  
FT TRANSMEM 55 67 Potential.  
FT TRANSMEM 70 85 Potential.  
FT TRANSMEM 97 107 Potential.  
FT TRANSMEM 111 126 Potential.  
FT TRANSMEM 146 157 Potential.  
FT TRANSMEM 163 179 Potential.  
FT TRANSMEM 185 196 Potential.  
FT REPEAT 205 206 1.  
FT REPEAT 207 208 2.  
FT REPEAT 209 210 3.  
FT REPEAT 211 212 4.  
FT DOMAIN 214 342 OmpA-like.  
FT REGION 205 212 4 X 2 AA tandem repeats of A-P.  
FT DISULFID 315 327 By similarity.  
FT CONFLICT 114 114 V -> F (in Ref. 1).  
FT CONFLICT 247 247 S -> I (in Ref. 1).  
SQ SEQUENCE 350 AA; 37515 MW; B4AC52C8C5DF54FE CRC64;  
  
Query Match 82.0%; Score 1495; DB 1; Length 350;  
Best Local Similarity 82.8%; Pred. No. 2e-106;  
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;  
  
QY 6 VLNAAPKNTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVNPYLG 65  
DB 18 VAQAAPKNTWYAGKLGWSQYHDTGFI-----HNDGPTHENQLGAGAFGGYQVNPY 72  
  
QY 66 EMGYDWMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLLGGMWRADSKGN 125  
DB 73 EMGYDWMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLLGGMWRADSKSN 132

QY 126 STGVSRSEHDTGVSVPFAGGVEMAVTRDIATRLVYQWVNNIGDAGTVGTDPDNGMLSLGV 185  
DB 133 G-GPSTKDHDTGVSVPFAGGIYAITPEIATRLVYQWVNNIGDANTIGTRPDNGLLSGV 191  
  
QY 186 SYRFGQEDAAPVAPAPAPAPAPAPVATKHFTELKSDVLFNFNFKATLKPEGQALDQLYTQLSN 245  
DB 192 SYRFGQEAAPVAPAPAPAPAPAPVATKHFTELKSDVLFNFNFKSTLKPEGQALDQLYSOLSN 251  
  
QY 246 MPFKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGHGESNPVT 305  
DB 252 LDPKDGSSVVLGFTDRIGSDAYNQQLSEKRAQSVVDYLISKGIPSKISARGHGESNPVT 311  
  
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVWVTP 342  
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKYKDVVWVTP 348  
  
RESULT 14  
Q8CW76 ECOL6  
ID Q8CW76\_ECOL6 PRELIMINARY; PRT; 379 AA.  
AC Q8CW76;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Outer membrane protein A.  
GN Name=ompA; OrderedLocustNames=c1093;  
OS Escherichia coli O6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=217992;  
RN [1]\_SEQUENCE  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=O6:Hi / CFT073 / ATCC 700928 / UPBC;  
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
RT of uropathogenic Escherichia coli.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).  
DR EMBL; AB016758; AAN79561.1; -; Genomic\_DNA.  
DR HSSP; P02934; 1QJP.  
DR SMR; Q8CW76; 51-230.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR006664; Bac\_OmpA.  
DR InterPro; IPR001035; MotY.  
DR InterPro; IPR002368; OmpA.  
DR InterPro; IPR006665; OmpA/MotB.  
DR InterPro; IPR006690; OMPA LIKE.  
DR InterPro; IPR000498; OmpA\_tmemb.  
DR Pfam; PF00691; OmpA; 1.  
DR Pfam; PF01389; OmpA membrane; 1.  
DR PRINTS; PR01023; NAFUGMOTY.  
DR PRINTS; PR01021; OMPADOMAIN.  
DR PRINTS; PR01022; OUTRMMBRANE.  
DR ProDom; PD000930; OmpA/MotB; 1.  
DR PROSITE; PS01068; OMPA; 1.  
KW Complete proteome.  
SQ SEQUENCE 379 AA; 41054 MW; CE396D152EB1EDCA CRC64;  
  
Query Match 81.6%; Score 1487; DB 2; Length 379;  
Best Local Similarity 83.7%; Pred. No. 9.4e-106;  
Matches 282; Conservative 17; Mismatches 32; Indels 6; Gaps 2;  
  
QY 6 VLNAAPKNTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVNPYLG 65  
DB 47 VAQAAPKNTWYAGKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPY 101  
  
QY 66 EMGYDWMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLLGGMWRADSKGN 125



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Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	1782	97.8	356	2	JC6558	outer membrane pro	
2	1542	84.6	350	2	S07222	outer membrane pro	
3	1525.5	83.7	351	1	MMEB4	outer membrane pro	
4	1511	82.9	346	1	MMEB4	outer membrane pro	
5	1511	82.9	346	2	A90759	outer membrane pro	
6	1511	82.9	346	2	G85622	outer membrane pro	
7	1499	82.2	350	2	A10626	outer membrane pro	
8	1490	81.7	350	1	MMEB4T	outer membrane pro	
9	1381.5	75.8	359	2	S07298	outer membrane pro	
10	1325.5	72.7	353	2	AD0175	probable outer mem	
11	1128.5	61.9	238	2	I62385	outer membrane pro	
12	1112.5	61.0	244	2	I62393	outer membrane pro	
13	1111	60.9	243	2	I62388	outer membrane pro	
14	1110.5	60.9	244	2	I62389	outer membrane pro	
15	1109	60.8	243	2	I84531	outer membrane pro	
16	1106	60.7	243	2	I62386	outer membrane pro	
17	1089	59.7	241	2	I62387	outer membrane pro	
18	1084	59.5	241	2	I62391	outer membrane pro	
19	1074.5	58.9	240	2	I62394	outer membrane pro	
20	1056.5	58.0	238	2	I40703	outer membrane pro	
21	646.5	35.5	353	2	C64187	outer membrane pro	
22	515	28.3	349	2	E84968	outer membrane pro	
23	443.5	24.3	321	2	F82104	outer membrane pro	
24	271	14.9	194	2	A45275	21k outer membrane	
25	262	14.4	236	2	A27894	outer membrane pro	
26	255	14.0	242	2	C81205	outer membrane cla	
27	251	13.8	240	2	A37004	outer membrane cla	
28	250	13.7	242	2	A81782	outer membrane pro	
29	243	13.3	326	2	S20494	root adhesin - Pse	



A;Experimental source: strain O157:H7, substrain RMD 05099S2  
C;Genetics:  
A;Gene: ECol1041  
C;Superfamily: outer membrane protein A

Query Match 82.9%; Score 1511; DB 2; Length 346;  
Best Local Similarity 84.9%; Pred. No. 3.9e-107;  
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTWYAGGKLGSQYHDTGYNGGFONNNGPTRNDOLGAGAFGGYQVNPYLGF 65  
DB 18 VAQAAPKDNWTWYTGAKLGSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVP 72  
QY 66 EMGYDMLGRMAYKGSVDNGAFKAQGVLTAKLGPITDDLDIYTRLGGMYMRADSKGNYA 125  
DB 73 EMGYDMLGRMPYKGSVENGA YKAQGVLTAKLGPITDDLDIYTRLGGMYMRADTKSN-- 130  
QY 126 STCVSRSEHDTGVSVPFAGGVAVTRDTATRLLEYQWVNIGDAGTVGTTPDNGMLS LGV 185  
DB 131 ---VYGKNHDTGVSVPFAGGVAVTPEIATRLEYQWVNIGDAHTIGTRPDNGMLS LGV 187  
QY 186 SYRFGGEDAAPVVAPAPAPEVATKHFTLKSDVLFNFNKATILKPEGQALDOLYTOLS N 245  
DB 188 SYRFGGEAAPVVAPAPAPEVQT KHTLUKSDVLFNFNKATILKPEGQALDDQYSQS N 247  
QY 246 MDPKDGSVVLYGTYDRIGSAYNQQLSEKRAQSWDYLVAKGIPAGKISARGMGESNPVT 305  
DB 248 LDPKDGSVVLYGTYDRIGSDAYNQGLSERPAQSVVDYLSKGIPADKISARGMGESNPVT 307  
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYEVVTTQP 342  
DB 308 GNTCDNVKORAALIDCLAPDRRVEIEVKGIKDVTTQP 344

RESULT 6  
G85622  
outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G85622  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: G85622  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-346 <STO>  
A;Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:AB005174; NID:g12  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: ompA  
C;Superfamily: outer membrane protein A

Query Match 82.9%; Score 1511; DB 2; Length 346;  
Best Local Similarity 84.9%; Pred. No. 3.9e-107;  
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTWYAGGKLGSQYHDTGYNGGFONNNGPTRNDOLGAGAFGGYQVNPYLGF 65  
DB 18 VAQAAPKDNWTWYTGAKLGSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVP 72  
QY 66 EMGYDMLGRMAYKGSVDNGAFKAQGVLTAKLGPITDDLDIYTRLGGMYMRADSKGNYA 125  
DB 73 EMGYDMLGRMPYKGSVENGA YKAQGVLTAKLGPITDDLDIYTRLGGMYMRADTKSN-- 130  
QY 126 STCVSRSEHDTGVSVPFAGGVAVTRDTATRLLEYQWVNIGDAGTVGTTPDNGMLS LGV 185  
DB 131 ---VYGKNHDTGVSVPFAGGVAVTPEIATRLEYQWVNIGDAHTIGTRPDNGMLS LGV 187  
QY 186 SYRFGGEDAAPVVAPAPAPEVATKHFTLKSDVLFNFNKATILKPEGQALDOLYTOLS N 245



Best Local Similarity 78.2%; Pred. No. 2.7e-97;  
Matches 269; Conservative 24; Mismatches 44; Indels 7; Gaps 4;

QY 6 VLNAAPKNDTWYAGGKLGWSQYHDTGYGNGFQ--NNGPTRNDOLGAGAGGQYQVNPYL 63  
DB 18 VAQAAPKNDTWYTGAKLGNQYHDTGYGNGYNGINGPHTKDKLQAGAGFLGQANQYL 77

QY 64 GFEMGYDLMGRMAYKGSVDNGAFKAGQVQLTAKLGYPTDLDIYTRLGGMWRADSKGN 123  
DB 78 GFELGYDLMGRMPYKGSVWNGAFKAGQVQLAALKLSYPIADLDIYTRLGGMWRADSKAN 137

QY 124 YASTGVSRSSEHDTGVSVPFAGGVWAVTRDIATRLFYQWNNIGDAGTGTTRPDNGMLSL 183  
DB 138 YGRTGQRLSDHDTGVSPLAAGVEYALTQKWATRLDYQVSNIGDAGTGTGARDPNTWLSL 197

QY 184 GVSYRFGQED--AAPVVAAPAPAPAEVATKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 242  
DB 198 GVSYRFGQDDVAP--APAPAPAPVETKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 255

QY 243 LSNMPPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302  
DB 256 LSNMPPKGSVAVLGYTDAVGSQYQNLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 315

QY 303 PVTGNTCDNVKARA--ALIDCLAPDRRVEIEVKGYKEVVTQAP 344  
DB 316 AVTGNTCGYKSGRATKAQIVCLAPDRRVEIEVKGYKEVVTQAPQ 359

RESULT 10  
AD0175  
probable outer membrane porin A protein ompA [imported] - Yersinia pestis (strain C092)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AD0175  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-farraga, A.M.; Chillingworth, T.; Cronan, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AD0175  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-353 <RES>  
A;Cross-references: UNIPROT:Q8ZG77; UNIPARC:UPI00000CD7EA; GB:AL590842; PIDN:CAC90263.1;  
C;Genetics:  
A;Gene: ompA  
C;Superfamily: outer membrane protein A

Query Match 72.7%; Score 1325.5; DB 2; Length 353;  
Best Local Similarity 75.2%; Pred. No. 4.8e-93;  
Matches 255; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

QY 6 VLNAAPKNDTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDOLGAGAGGQYQVNPYLGF 65  
DB 18 VAQAAPKNDTWYTGAKLGNQYHDTGYGNGYNGINGPHTKDKLQAGAGFLGQANQYLGF 73

QY 66 EMGYDLMGRMAYKGSVDNGAFKAGQVQLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125  
DB 74 EMGYDLMGRMPYKGSVWNGAFKAGQVQLAALKLSYPIADLDIYTRLGGMWRADSKGSP- 132

QY 126 STGVSRSSEHDTGVSVPFAGGVWAVTRDIATRLFYQWNNIGDAGTGTTRPDNGMLSL 184  
DB 133 DGGLDRASGHDTGVSPLVALGABYAWTKWATRMVQWNNIGDRETGVARNPGLLSVG 192

QY 185 VSYRFGQED--AAPVVAAPAPAPAEVATKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 243  
DB 193 VSYRFGQEDAAAPVAPTAPAPAPVDTKFTLKSVDVLFNFKATLKPEGQALDQLYAQL 252

QY 244 SNMPPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNP 303  
DB 253 SSIDPPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNP 312

QY 304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQAP 342  
DB 313 VTGNTCDNVKAPRAALIECLAPDRRVEIEVKGYKEVVTQAP 351

RESULT 11  
I62385  
outer membrane protein ompA - Escherichia vulneris (fragment)  
N;Alternate names: outer membrane protein II  
C;Species: Escherichia vulneris  
C;Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: I62385  
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A;Title: Molecular and evolutionary relationships among enteric bacteria.  
A;Reference number: I40701; MUID:92065252; PMID:1955870  
A;Accession: I62385  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-238 <RES>  
A;Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB:M63348; NID:q146984; PIDN:  
C;Genetics:  
A;Gene: ompA  
C;Superfamily: outer membrane protein A  
C;Keywords: membrane protein  
F;98-109/Region: alanine/proline-rich

Query Match 61.9%; Score 1128.5; DB 2; Length 238;  
Best Local Similarity 90.1%; Pred. No. 2.5e-78;  
Matches 219; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 93 LTAKLGPITDLDIYTRLGGMWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVWAVTR 152  
DB 1 LTAKLGPITDLDIYTRLGGMWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVWAVTR 55

QY 153 DIATRLFYQWNNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAAPVVAAPAPAEVATKH 212  
DB 56 DIATRLFYQWNNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAAPVVAAPAPAEVATKH 115

QY 213 FTLSKSDVLFNFKATLKPEGQALDQLYTQLSNMPPKGSVAVLGYTDRIGSEAYNQOLS 272  
DB 116 FTLSKSDVLFNFKATLKPEGQALDQLYTQLSNMPPKGSVAVLGYTDRIGSEAYNQOLS 175

QY 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332  
DB 176 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 235

QY 333 KGY 335  
DB 236 KGY 238

RESULT 12  
I62393  
outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)  
N;Alternate names: outer membrane protein II  
C;Species: Escherichia vulneris  
A;Variety: ATCC 33822  
C;Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: I62393  
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A;Title: Molecular and evolutionary relationships among enteric bacteria.  
A;Reference number: I40701; MUID:92065252; PMID:1955870  
A;Accession: I62393  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-244 <RES>  
A;Cross-references: UNIPROT:Q47880; UNIPARC:UPI00000B0580; GB:M63350; NID:q147000; PIDN:  
C;Experimental source: ATCC 33822  
C;Genetics:  
A;Gene: ompA  
C;Superfamily: outer membrane protein A

C;Keywords: membrane protein	
F;104-115/Region: alanine/proline-rich	
Query Match	61.0%; Score 1112.5; DB 2; Length 244;
Best Local Similarity	87.2%; Pred. No. 4.2e-77;
Matches	212; Conservative 15; Mismatches 15; Indels 1; Gaps 1;
QY	93 LTAALGVPIITDDLDIYTRLCGMVWRADSKGNVASTGVSRSEHDTGSPVPAGGVEAVATR 152
Db	1 LTAALGVPIITDDLDIYTRLCGMVWRADSKAQVPGTGASFKDHDGTGSPVPAGGVEAVATR 60
QY	153 DIATRLVQWNNIGDAGTGTGTRPDNGMLSLGVSYRFG-QEDAAPVAVAPAPAPAVATK 211
Db	61 DIATRLVQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDVAVVAVAPAPAPAVATK 120
QY	212 HFTLKSDVLFNFNPKATLKPEGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSEAYNQGL 271
Db	121 HFTLKSDVLFNFNPKATLKPEGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSDAYNQGL 180
QY	272 SEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
Db	181 SEKRAQSVVDYLSKGIPIKSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240
332 VKG 334	
241 VKG 243	
RESULT 13	
I62388	
outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)	
N;Alternate names: outer membrane protein II	
C;Species: Escherichia fergusonii	
A;Variety: ATCC 35472	
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
A;Title: Molecular and evolutionary relationships among enteric bacteria.	
A;Reference number: 140701; PMID:92065252; PMID:1955870	
A;Accession: I62388	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-243 <RES>	
A;Cross-references: UNIPROT:P24747; UNIPARC:UPI0000130CF3; GB:M63352; NID:g146990; PIDN:	
A;Experimental source: ATCC 35471	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-243 <RE2>	
A;Cross-references: UNIPARC:UPI0000130CF3; GB:M63353; NID:g146998; PIDN:AAA24240.1; PID:	
A;Experimental source: ATCC 35472	
C;Genetics:	
A;Gene: ompA	
C;Superfamily: outer membrane protein A	
C;Keywords: membrane protein	
F;103-114/Region: alanine/proline-rich	
Query Match	60.9%; Score 1111; DB 2; Length 243;
Best Local Similarity	87.2%; Pred. No. 5.5e-77;
Matches	211; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY	93 LTAALGVPIITDDLDIYTRLCGMVWRADSKGNVASTGVSRSEHDTGSPVPAGGVEAVATR 152
Db	1 LTAALGVPIITDDLDIYTRLCGMVWRADTKAHNNVTGESEKNHDTGSPVPAGGVEAVATP 60
QY	153 DIATRLVQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAPVAVAPAPAPAVATKH 212
Db	61 DIATRLVQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAPVAVAPAPAPAVATKH 120
QY	213 FTLKSDVLFNFNPKATLKPEGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSEAYNQGLS 272
Db	121 FTLKSDVLFNFNPKATLKPEGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSDAYNQGLS 180

QY	273 EKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 312
Db	181 EKRAQSVVDYLSKGIPIKSNKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 240
QY	333 KG 334
Db	241 KG 242
RESULT 14	
I62389	
outer membrane protein ompA - Escherichia vulneris (ATCC 33821) (fragment)	
N;Alternate names: outer membrane protein II	
C;Species: Escherichia vulneris	
A;Variety: ATCC 33821	
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
A;Title: Molecular and evolutionary relationships among enteric bacteria.	
A;Reference number: 140701; PMID:92065252; PMID:1955870	
A;Accession: I62389	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-244 <RES>	
A;Cross-references: UNIPROT:Q99115; UNIPARC:UPI00000BBF1D; GB:M63349; NID:g146992; PIDN:	
A;Experimental source: ATCC 33821	
C;Genetics:	
A;Gene: ompA	
C;Superfamily: outer membrane protein A	
C;Keywords: membrane protein	
F;104-115/Region: alanine/proline-rich	
Query Match	60.9%; Score 1110.5; DB 2; Length 244;
Best Local Similarity	86.8%; Pred. No. 6e-77;
Matches	211; Conservative 16; Mismatches 15; Indels 1; Gaps 1;
QY	93 LTAALGVPIITDDLDIYTRLCGMVWRADSKGNVASTGVSRSEHDTGSPVPAGGVEAVATR 152
Db	1 LTAALGVPIITDDLDIYTRLCGMVWRADAKSPQGGTGASPKDHDGTGSPVPAGGVEAVATR 60
QY	153 DIATRLVQWNNIGDAGTGTGTRPDNGMLSLGVSYRFG-QEDAAPVAVAPAPAPAVATK 211
Db	61 DIATRLVQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDVAVVAVAPAPAPAVATK 120
QY	212 HFTLKSDVLFNFNPKATLKPEGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSEAYNQGL 271
Db	121 HFTLKSDVLFNFNPKATLKPEGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSDAYNQGL 180
QY	272 SEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
Db	181 SEKRAQSVVDYLSKGIPIKSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240
332 VKG 334	
241 VKG 243	
RESULT 15	
I84531	
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)	
N;Alternate names: outer membrane protein II	
C;Species: Escherichia fergusonii	
A;Variety: ATCC 35469	
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
A;Title: Molecular and evolutionary relationships among enteric bacteria.	
A;Reference number: 140701; PMID:92065252; PMID:1955870	
A;Accession: I84531	
A;Status: preliminary; translated from GB/EMBL/DBJ	



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